

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21	100.0	195	2 US-09-485-657A-14	Sequence 14, App1
C 2	21	100.0	195	4 US-09-366-380-14	Sequence 14, App1
C 3	21	100.0	195	5 PCT-US95-02303-14	Sequence 14, App1
C 4	21	100.0	1648	4 US-09-659-791A-13	Sequence 13, App1
C 5	21	100.0	1651	4 US-09-659-791A-13	Sequence 13, App1
C 6	21	100.0	7610	4 US-09-659-791A-12	Sequence 12, App1
C 7	19.4	92.4	181	2 US-08-485-657A-19	Sequence 19, App1
C 8	19.4	92.4	181	4 US-09-366-380-19	Sequence 18, App1
C 9	19.4	92.4	181	5 PCT-US95-02303-18	Sequence 18, App1
C 10	15.2	72.4	6671	1 US-08-280-443-1	Sequence 1, App1
C 11	15.2	72.4	6671	1 US-08-457-459-1	Sequence 1, App1
C 12	15.2	72.4	6671	3 US-09-187-331-4	Sequence 4, App1
C 13	15.2	72.4	6671	5 PCT-US95-02275-1	Sequence 31, App1
C 14	15.2	72.4	6756	1 US-08-151-74-31	Sequence 31, App1
C 15	15.2	72.4	6756	2 US-08-419-448-31	Sequence 31, App1
C 16	15.2	72.4	6756	4 US-09-233-510-31	Sequence 31, App1
C 17	14.8	70.5	1438	3 US-09-103-840A-2	Sequence 4, App1
C 18	14.8	70.5	1438	4 US-09-470-946-4	Sequence 20, App1
C 19	14.8	70.5	3563	3 US-09-041-886-20	Sequence 5, App1
C 20	14.8	70.5	3596	2 US-08-779-801-5	Sequence 5, App1
C 21	14.8	70.5	3596	4 US-09-298-441-5	Sequence 2, App1
C 22	14.8	70.5	4403765	3 US-09-103-840A-2	Sequence 1, App1
C 23	14.8	70.5	4411529	3 US-09-103-840A-1	Sequence 22,7, Ap
C 24	14.6	69.5	885	4 US-09-252-991A-1618	Sequence 1, App1
C 25	14.6	69.5	1080	4 US-09-252-991A-2217	Sequence 22,7, Ap
C 26	14.6	69.5	1219	4 US-09-192-012-1	Sequence 22,5, Ap
C 27	14.6	69.5	2139	4 US-09-252-991A-2295	Sequence 22,5, Ap

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/podata/2/ina/5A COMB.seq:*

2: /cgn2_6/podata/2/ina/5B COMB. seq:*

3: /cgn2_6/podata/2/ina/6A COMB. seq:*

4: /cgn2_6/podata/2/ina/6B COMB. seq:*

5: /cgn2_6/podata/2/ina/PCFTUS COMB.seq:*

6: /cgn2_6/podata/2/ina/backfile1.seq:*

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21	100.0	195	2 US-09-485-657A-14	Sequence 14, App1
C 2	21	100.0	195	4 US-09-366-380-14	Sequence 14, App1
C 3	21	100.0	195	5 PCT-US95-02303-14	Sequence 14, App1
C 4	21	100.0	1648	4 US-09-659-791A-13	Sequence 13, App1
C 5	21	100.0	1651	4 US-09-659-791A-13	Sequence 13, App1
C 6	21	100.0	7610	4 US-09-659-791A-12	Sequence 12, App1
C 7	19.4	92.4	181	2 US-08-485-657A-19	Sequence 19, App1
C 8	19.4	92.4	181	4 US-09-366-380-19	Sequence 18, App1
C 9	19.4	92.4	181	5 PCT-US95-02303-18	Sequence 18, App1
C 10	15.2	72.4	6671	1 US-08-280-443-1	Sequence 1, App1
C 11	15.2	72.4	6671	1 US-08-457-459-1	Sequence 1, App1
C 12	15.2	72.4	6671	3 US-09-187-331-4	Sequence 4, App1
C 13	15.2	72.4	6671	5 PCT-US95-02275-1	Sequence 31, App1
C 14	15.2	72.4	6756	1 US-08-151-74-31	Sequence 31, App1
C 15	15.2	72.4	6756	2 US-08-419-448-31	Sequence 31, App1
C 16	15.2	72.4	6756	4 US-09-233-510-31	Sequence 31, App1
C 17	14.8	70.5	1438	3 US-09-103-840A-2	Sequence 4, App1
C 18	14.8	70.5	1438	4 US-09-470-946-4	Sequence 20, App1
C 19	14.8	70.5	3563	3 US-09-041-886-20	Sequence 5, App1
C 20	14.8	70.5	3596	2 US-08-779-801-5	Sequence 5, App1
C 21	14.8	70.5	3596	4 US-09-298-441-5	Sequence 2, App1
C 22	14.8	70.5	4403765	3 US-09-103-840A-2	Sequence 1, App1
C 23	14.8	70.5	4411529	3 US-09-103-840A-1	Sequence 22,7, Ap
C 24	14.6	69.5	885	4 US-09-252-991A-1618	Sequence 22,7, Ap
C 25	14.6	69.5	1080	4 US-09-252-991A-2217	Sequence 22,7, Ap
C 26	14.6	69.5	1219	4 US-09-192-012-1	Sequence 22,5, Ap
C 27	14.6	69.5	2139	4 US-09-252-991A-2295	Sequence 22,5, Ap

Qy 1 ATGTCTGAGACCGTCGTC 21

Qy 1 ATTGTCTGAGACCGTCGTC 21

ALIGNMENTS

RESULT 1
US-08-485-657A-14/C
Sequence 14, Application US/08485657A
; General Information:
; Patent No. 5942399
; Inventor: Kirschling, Deborah J
; Applicant: Guidkov, Andrei
; Applicant: Robinson, Igor B
; Title of Invention: Genes and Genetic Elements Associated
; with Sensitivity to Cisplatin
; Number of Sequences: 23
; Correspondence Address:
; Addressee: McDonnell Boehnen Hulbert & Berghoff
; Street: 300 South Wacker Drive, 32nd Floor
; City: Chicago
; State: Illinois
; Country: USA
; Zip: 60606
; Computer Readable Form:
; Medium Type: Floppy disk
; Computer: IBM PC Compatible
; Operating System: PC-DOS/MS-DOS
; Software: PatentIn Release #1.0, Version #1.25
; Current Application Data:
; Application Number: US/08/485, 657A
; Filing Date: 07-JUN-1995
; Classification: 800
; Attorney/Agent Information:
; Name: No. 5942389nan, Kevin E
; Registration Number: 35, 303
; Reference/Docket Number: 93, 354-N
; Telecommunication Information:
; Telephone: 312-913-0001
; Telefax: 312-913-0002
; Telex:
; Information for Seq ID No. 14:
; Sequence Characteristics:
; Length: 195 base Pairs
; Strandedness: single
; Topology: linear
; Molecule Type: cDNA
; Type: nucleic acid
; Query Match 100.0%; Score 21; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.05%; Mismatches 0; Indels 0; Gaps 0;

Db 153 ATTGTCTGAGACCGCTGGTC 133

RESULT 2

US-09-366-380-14/c

Sequence 14, Application US/09366380

Patent No. 6541603

GENERAL INFORMATION:

APPLICANT: Kirschling, Deborah J

APPLICANT: Gudkov, Andrei

APPLICANT: Roninson, Igor B

TITLE OF INVENTION: Genes and Genetic Elements Associated with Sensitivity to Cisplatin

NUMBER OF SEQUENCES: 23

RESPONSEE: McDonnell Boehnen Hulbert & Berghoff

STREET: 300 South Wacker Drive, 32nd Floor

STATE: Chicago

COUNTRY: Illinois

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/366-380

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/199,900

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: No. 6541603nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 93,354-N

TELEPHONE: 312-913-0001

TELEFAX: 312-913-0002

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 195 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-09-366-380-14

Query Match 100.0%; Score 21; DB 4; Length 195;

Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGTCTGAGACCGCTGGTC 21

Db 153 ATTGTCTGAGACCGCTGGTC 133

RESULT 3

PCT-US95-02303-14/c

Sequence 14, Application PC/US95/02303

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Genes and Genetic Elements Associated with Sensitivity to Cisplatin

NUMBER OF SEQUENCES: 25

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/659,791A

SEQUENCE 3, Application US/09659791A

Patent No. 6393808

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Susan M. Freier

TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION

FILE REFERENCE: RTS-0156

CURRENT APPLICATION NUMBER: US/09/659,791A

CURRENT FILING DATE: 2000-09-11

NUMBER OF SEQ ID NOS: 90

SEQ ID NO 3

LENGTH: 1648

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (53) . . . (1402)

US-09-659-791A-3

Query Match 100.0%; Score 21; DB 4; Length 1648;

Best Local Similarity 100.0%; Pred. No. 0.072;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGTCTGAGACCGCTGGTC 21

Db 153 ATTGTCTGAGACCGCTGGTC 133

RESULT 4

US-09-659-791A-3/c

Sequence 3, Application US/09659791A

Patent No. 6393808

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Susan M. Freier

TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION

FILE REFERENCE: RTS-0156

CURRENT APPLICATION NUMBER: US/09/659,791A

CURRENT FILING DATE: 2000-09-11

NUMBER OF SEQ ID NOS: 90

SEQ ID NO 13

LENGTH: 1651

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (199) . . . (1545)

US-09-659-791A-3

Query Match 100.0%; Score 21; DB 4; Length 1651;

Best Local Similarity 100.0%; Pred. No. 0.072;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGTCTGAGACCGCTGGTC 21

Db 153 ATTGTCTGAGACCGCTGGTC 133

RESULT 5

US-09-659-791A-13/c

Sequence 13, Application US/09659791A

Patent No. 6393808

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Susan M. Freier

TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION

FILE REFERENCE: RTS-0156

CURRENT APPLICATION NUMBER: US/09/659,791A

CURRENT FILING DATE: 2000-09-11

NUMBER OF SEQ ID NOS: 90

SEQ ID NO 13

LENGTH: 1651

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (199) . . . (1545)

US-09-659-791A-13

Query Match 100.0%; Score 21; DB 4; Length 1651;

Best Local Similarity 100.0%; Pred. No. 0.072;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGTCTGAGACCGTCTGGTC 21
 Db 292 ATTGTCTGAGACCGTCTGGTC 262

RESULT 6
 US-09-659-791A-12/C
 Sequence 12, Application US/09659791A
 GENERAL INFORMATION:
 APPLICANT: Susan M. Freier
 TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
 FILE REFERENCE: RTS-0156
 CURRENT APPLICATION NUMBER: US/09/659,791A
 CURRENT FILING DATE: 2000-09-11
 NUMBER OF SEQ ID NOS: 90
 SEQ ID NO: 12
 LENGTH: 7610
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: unsure
 LOCATION: 5461
 OTHER INFORMATION: unknown
 NAME/KEY: unsure
 LOCATION: 5462
 OTHER INFORMATION: unknown
 US-09-659-791A-12

Query Match 100.0%; Score 21; DB 4; Length 7610;
 Best Local Similarity 100.0%; Pred. No. 0.093;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGTCTGAGACCGTCTGGTC 21
 Db 5624 ATTGTCTGAGACCGTCTGGTC 5604

RESULT 7
 US-08-485-657A-19/C
 Sequence 19, Application US/08485657A
 GENERAL INFORMATION:
 Patent No. 5942389
 APPLICANT: Kirschling, Deborah J
 APPLICANT: Gudkov, Andrei
 APPLICANT: Roninson, Igor B
 TITLE OF INVENTION: Genes and Genetic Elements Associated
 WITH SENSITIVITY TO CISPLATIN
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 STREET: McDonnell Boehnen Hulbert & Berghoff
 STREET: 300 South Wacker Drive, 32nd Floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/366,380
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 6541603nan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 93,354-N
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-913-0001
 TELEFAX: 312-913-0002
 TELEX:

INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 181 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-485-657A-19

Query Match 92.4%; Score 19.4%; DB 4; Length 181;
 Best Local Similarity 95.2%; Pred. No. 0.34%;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATTGTCTGAGACCGTCTGGTC 21
 Db 139 ATTGTCTGAGACCGTCTGGTC 119

RESULT 8
 US-09-366-380-19/C
 Sequence 19, Application US/09366380
 / Patient No. 6541603
 / GENERAL INFORMATION:
 / APPLICANT: Kirschling, Deborah J
 / APPLICANT: Gudkov, Andrei
 / APPLICANT: Roninson, Igor B
 / TITLE OF INVENTION: Genes and Genetic Elements Associated
 / WITH SENSITIVITY TO CISPLATIN
 / NUMBER OF SEQUENCES: 23
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
 / STREET: 300 South Wacker Drive, 32nd Floor
 / CITY: Chicago
 / STATE: Illinois
 / COUNTRY: USA
 / ZIP: 60606
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/366,380
 / FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: No. 6541603nan, Kevin E
 / REGISTRATION NUMBER: 35,303
 / REFERENCE/DOCKET NUMBER: 93,354-N
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 312-913-0001
 / TELEFAX: 312-913-0002
 / TELEX:
 / INFORMATION FOR SEQ ID NO: 19:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 181 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / MOLECULE TYPE: cDNA
 / US-09-366-380-19

Query Match 92.4%; Score 19.4%; DB 4; Length 181;
 Best Local Similarity 95.2%; Pred. No. 0.34%;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATTGTCTGAGACCGTCTGGTC 21
 Db 139 ATTGTCTGAGACCGTCTGGTC 119

Db 139 ATGGCTGAGACCGTCTGGTC 119

RESULT 9
PCT-US95-02303-18/C
Sequence 18, Application PC/TUS9502303

GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: Genes and Genetic Elements Associated with Sensitivity to Cisplatin
NUMBER OF SEQUENCES: 25

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02303

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
PCT-US95-02303-18

Query Match 92.4%; Score 19 4; DB 5; Length 181;
Best Local Similarity 95.2%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 139 ATGGCTGAGACCGTCTGGTC 119

RESULT 10
US-08-280-457-1/c
Sequence 1, Application US/08280443
Patent No. 5643778

GENERAL INFORMATION:

APPLICANT: Nishikura, Kazuko
TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use
NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,459
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/197,794
CLASSIFICATION: 435
FILING DATE: 17-FEB-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/280,443
FILING DATE: 25-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST49USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6671 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 155..3832

Query Match 72.4%; Score 15 2; DB 1; Length 6671;
Best Local Similarity 85.0%; Pred. No. 98;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

US-08-457-457-1

GENERAL INFORMATION:

APPLICANT: Nishikura, Kazuko
APPLICATION NUMBER: US 08/197,794
FILING DATE: 17-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST49USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6671 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 155..3832

Query Match 72.4%; Score 15 2; DB 1; Length 6671;
Best Local Similarity 85.0%; Pred. No. 98;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGCTGAAACCGCTGGTC 21
 US-08-555-678-1/c
 Sequence 1, Application US/08555578
 Patent No. 5763174

GENERAL INFORMATION:
 APPLICANT: Nishikura, Kaiko
 TITLE OF INVENTION: RNA Editing Enzyme and Methods
 TITLE OF INVENTION: of Use Thereof
 NUMBER OF SEQUENCES: 67
 CORRESPONDENCE ADDRESS:
 STREET: Howson and Howson
 STREET: Spring House Corporate Cntr, P.O. Box 457
 CITY: Spring House
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19477

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/555,678
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/197,794
 FILING DATE: 17-FEB-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/280,443
 FILING DATE: 25-JUL-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/457,459
 FILING DATE: 01-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Bak, Mary E.
 REGISTRATION NUMBER: 31,215
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-540-9206
 FAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6671 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: unknown
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 155..3832

RESULT 13
 US-08-555-678-1
 Query Match 72.4%; Score 15.2; DB 1; Length 6671;
 Best Local Similarity 85.0%; Pred. No. 98;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 STRANDEDNESS: double
 LENGTH: 6671 base pairs
 TYPE: nucleic acid
 TOPOLOGY: unknown
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 155..3832

US-08-555-678-1/c

Sequence 1, Application PC/TUS95/02275

GENERAL INFORMATION:

APPLICANT: Wistar Institute of Anatomy & Biology
 TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use

TITLE OF INVENTION: Thereof
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Howson and Howson
 STREET: Spring House Corporate Cntr, P.O. Box 457
 CITY: Spring House
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19477
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/02275
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/280,443
 FILING DATE: 25-JUL-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/197,794
 FILING DATE: 17-FEB-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Bak, Mary E.
 REGISTRATION NUMBER: 31,215
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-540-9206
 FAX: 215-540-5818
 IN INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6671 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: unknown
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 155..3832

RESULT 14
 US-08-151-574-31
 Sequence 31, Application US/08151574
 Patent No. 5436156
 GENERAL INFORMATION:
 APPLICANT: Robert F.M. Van Gorcom
 APPLICANT: Robert F.M. Van Gorcom
 APPLICANT: Willem Van Hartingsveldt
 APPLICANT: Petrus A. Van Paridon
 APPLICANT: Anemarie E. Veenstra
 APPLICANT: Rudolf G.M. Lutten
 APPLICANT: Gerardus Seletten
 TITLE OF INVENTION: Cloning and Expression of Microbial
 TITLE OF INVENTION: Cloning and Expression of Microbial
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morrison & Foerster
 STREET: 545 Middlefield Road, Suite 200
 CITY: Menlo Park
 STATE: California
 COUNTRY: USA
 ZIP: 94025-3471

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/151,574
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/688,578
 FILING DATE: 24 MAY 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Murashige, Kate H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 24615-20026.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-327-7250
 SEQUENCE FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6756 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Aspergillus ficuum (Aspergillus niger)
 STRAIN: NERL 3135

IMMEDIATE SOURCE:
 LIBRARY: lambda AF
 CLONE: pAF2-3, pAF2-6, pAF2-7

FEATURE:
 NAME/KEY: exon
 LOCATION: 210..253
 FEATURE:
 NAME/KEY: intron
 LOCATION: 254..355
 FEATURE:
 NAME/KEY: exon
 LOCATION: 356..1715
 FEATURE:
 NAME/KEY: CDS
 LOCATION: join(210..253, 356..1715)
 OTHER INFORMATION: /codon_start= 210
 OTHER INFORMATION: /product= "Phytase"

FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 210..380
 NAME/KEY: mat_peptide
 LOCATION: 381..1712
 IDENTIFICATION METHOD: experimental
 OTHER INFORMATION: /function= "inositol phosphate phosphatase"
 OTHER INFORMATION: /product= "Phytase"
 OTHER INFORMATION: /product= "Phytase"
 OTHER INFORMATION: /evidence= EXPERIMENTAL
 US-08-151-574-31

Query Match 2 TGTCTAGACCTCTCGTC 21
 Best Local Similarity 85.0% Score 15.2; DB 1; Length 6756;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGTCTAGACCTCTCGTC 21
 Db 130 TTATATGAGCCGTCGGTC 149

RESULT 15 US-08-419-448-31
 Sequence 31, Application US/08419448

Patent No. 5863533
 GENERAL INFORMATION:
 APPLICANT: Robert P.M. Van Gorcom
 APPLICANT: Willem Van Hartingsveldt
 APPLICANT: Petrus A. Van Paridon
 APPLICANT: Anemarie E. Veenstra
 APPLICANT: Rudolf G.M. Luttin
 APPLICANT: Gerardus Seiten
 TITLE OF INVENTION: Cloning and Expression of Microbial
 TITLE OF INVENTION: Phytase
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Morrison & Foerster
 STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006-1888
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/419,448
 FILING DATE: 10 APR 1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Murashige, Kate H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 24615-20026.10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-887-1500
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6756 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Aspergillus ficuum (Aspergillus niger)
 STRAIN: NERL 3135
 IMMEDIATE SOURCE:
 LIBRARY: lambda AF
 CLONE: pAF2-3, pAF2-6, pAF2-7
 FEATURE:
 NAME/KEY: exon
 LOCATION: 210..253
 FEATURE:
 NAME/KEY: intron
 LOCATION: 254..355
 FEATURE:
 NAME/KEY: exon
 LOCATION: 356..1715
 FEATURE:
 NAME/KEY: CDS
 LOCATION: join(210..253, 356..1715)
 OTHER INFORMATION: /codon_start= 210
 OTHER INFORMATION: /product= "Phytase"

FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 210..380
 NAME/KEY: mat_peptide
 LOCATION: 381..1712
 IDENTIFICATION METHOD: experimental
 OTHER INFORMATION: /function= "inositol phosphate phosphatase"
 OTHER INFORMATION: /product= "Phytase"
 OTHER INFORMATION: /product= "Phytase"
 OTHER INFORMATION: /product= "Phytase"

FEATURE:
 NAME/KEY: CDS
 LOCATION: join(210..253, 356..1715)
 OTHER INFORMATION: /codon_start= 210
 OTHER INFORMATION: /product= "Phytase"

FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 381..1712
 IDENTIFICATION METHOD: experimental
 OTHER INFORMATION: /function= "inositol phosphate phosphatase"
 OTHER INFORMATION: /product= "Phytase"

FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 210..380
 NAME/KEY: mat_peptide
 LOCATION: 381..1712
 IDENTIFICATION METHOD: experimental
 OTHER INFORMATION: /function= "inositol phosphate phosphatase"
 OTHER INFORMATION: /product= "Phytase"

OTHER INFORMATION: /evidence= EXPERIMENTAL

us-08-419-448-31

Query Match 72.4%; Score 15.2; DB 2; Length 6756;

Best Local Similarity 85.0%; Pred. No. 98; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 3;

Qy 2 TTGTCTGAAACCGTCGGTC 21

Db 130 TTATATGAAACCGTCGGTC 149

Search completed: January 21, 2004, 13:11:48;
Job time : 63 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw mode

Run on: January 21, 2004, 10:07:51 ; Search time 799.5 Seconds
(without alignments)
1074.549 Million cell updates/sec

Title: US-09-913-325-5

Perfect score: 21

Sequence: 1 atttgtctggaccgtctgttc 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEtbl1:
1: gb_ba:/*
2: gb_htg:/*
3: gb_in:/*
4: gb_cm:/*
5: gb_cv:/*
6: gb_dat:/*
7: gb_ph:/*
8: gb_D1:/*
9: gb_Dr:/*
10: gb_ro:/*
11: gb_sts:/*
12: gb_sy:/*
13: gb_un:/*
14: gb_vr:/*
15: em_ba:/*
16: em_fun:/*
17: em_hum:/*
18: em_in:/*
19: em_mu:/*
20: em_om:/*
21: em_or:/*
22: em_ov:/*
23: em_pat:/*
24: em_Ph:/*
25: em_P1:/*
26: em_ro:/*
27: em_sts:/*
28: em_un:/*
29: em_vr:/*
30: em_htg_hum:/*
31: em_htg_inv:/*
32: em_htg_other:/*
33: em_htg_mus:/*
34: em_htg_pln:/*
35: em_htg_rid:/*
36: em_htg_mam:/*
37: em_htg_vrt:/*
38: em_sy:/*
39: em_htgo_hum:/*
40: em_htgo_mus:/*
41: em_htgo_other:/*

Pre. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
c 1	21	100.0	195	6	AR302784		AR302784 Sequence
c 2	21	100.0	396	6	AX093197		AX093197 Sequence
c 3	21	100.0	482	6	BD117323		BD117323 EST and e
c 4	21	100.0	491	6	BD027496		BD027496 Sequence
c 5	21	100.0	512	6	BD071299		BD071299 Secreted
c 6	21	100.0	1589	6	AX600512		AX600512 Sequence
c 7	21	100.0	1648	6	AR208704		AR208704 Sequence
c 8	21	100.0	1648	9	HUMTRM2A		M64722 Human TRPM-2
c 9	21	100.0	1651	6	AR208714		AR208714 Sequence
c 10	21	100.0	1651	9	HUMCL1		M25915 Human comp1
c 11	21	100.0	1651	9	BC019588		Homo sapi
c 12	21	100.0	1658	9	BC019588		X14723 Human SP-40
c 13	21	100.0	1676	9	HSCSP0		AX202086 Sequence
c 14	21	100.0	1678	6	AX202086		BC010514 Homo sapi
c 15	21	100.0	1684	9	BC010514		BC010514 Homo sapi
c 16	21	100.0	1712	6	AX600509		AX600509 Sequence
c 17	21	100.0	7610	6	AR208713		AR208713 Sequence
c 18	21	100.0	7610	9	HUMTRM2A		M63276 Human TRPM-2
c 19	21	100.0	134514	2	AC025192		AC05192 Homo sapi
c 20	21	100.0	17457	9	AF235104		AF235104 Homo sapi
c 21	21	100.0	234431	9	AF311103		AF311103 Homo sapi
c 22	21	100.0	334051	2	AC123374		AC123374 Rattus no
c 23	20	95.2	1546	9	AK093399		AK093399 Homo sapi
c 24	20	92.4	181	6	AR302789		AR302789 Sequence
c 25	19.4	92.4	221	6	AX701616		AX701616 Sequence
c 26	17.8	84.8	66565	9	AC092103		AC092103 Homo sapi
c 27	17.8	84.8	136131	9	AC000360		AC000360 Homo sapi
c 28	17.8	84.8	147750	10	AC122503		AC122503 Mus muscu
c 29	17.8	84.8	173513	9	HSJ1059C8		Z98949 Human DNA S
c 30	17.8	84.8	180230	10	AC124692		AC124692 Mus muscu
c 31	17.8	84.8	111410	10	AC081814		AC081814 Mus muscu
c 32	17.8	84.8	27330	10	AC02786		AC02786 Mus muscu
c 33	17.8	84.8	288888	9	HSA311932		AJ310932 Homo sapi
c 34	17.4	82.9	127102	9	HSJ1059C8		AL078623 Human DNA
c 35	17.4	82.9	253726	2	AC094330		AC094330 Rattus no
c 36	17.4	82.9	256229	2	AC102656		AC102656 Mus muscu
c 37	17.4	82.9	241215	2	AC113683		AC094144 Rattus no
c 38	17.4	82.9	246769	2	AC094144		AC094144 Rattus no
c 39	17.4	82.9	262108	2	AC105555		AC105555 Rattus no
c 40	16.8	80.0	345	9	AY062323		AY062323 Homo sapi
c 41	16.8	80.0	1785	6	AX653339		AX653339 Sequence
c 42	16.8	80.0	10029	1	AB011998		AE011998 Xanthomonas campestris subsp. campestris
c 43	16.8	80.0	60786	2	AC123317		AC123317 Homo sapi
c 44	16.8	80.0	120879	9	AL445986		AL445986 Human DNA
c 45	16.8	80.0	138036	2	AP004762		AP004762 Oryza sativa L.

ALIGNMENTS

RESULT	1	AR302784/c	195 bp	mRNA	linear	PAT 12-JUN-2003
LOCUS		Sequence 14	From patent US 6541603.			
DEFINITION			Sequence 14			
ACCESSION		AR302784				
VERSION		AR302784.1				
KEYWORDS		GI:31691271				
SOURCE						
ORGANISM						
UNCLASSIFIED						
REFERENCE		1 (bases 1 to 195)				
AUTHORS		Kirschling, D.J.; Gudkov, A. and Roninson, I.B.				
TITLE		Genes and genetic elements associated with sensitivity to platinum-based drugs				
JOURNAL		Patent: US 6541603-A 14 01-APR-2003;				

FEATURES Location/Qualifiers
source 1. /organism="unknown"
BASE COUNT 46 a 45 c 71 g 33 t

Query Match 100.0%; Score 21; DB 6; Length 195;
Best Local Similarity 100.0%; Prod. No. 3.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTCTGAGACCGCTCTGGTC 21
Db 153 ATGGTCTGAGACCGCTCTGGTC 133

RESULT 2
AX093197/c
LOCUS 396 bp DNA
DEFINITION Sequence 15 from Patent WO0118046.
ACCESSION AX093197
VERSION AX093197.1 GI:13509646
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Chordata; Craniata; Buteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Buteleostomi; Homo.
REFERENCE 1. Xu,J. and Stolk,J.A.
AUTHORS
TITLE Ovarian tumor sequences and methods of use therefor
JOURNAL Patent: WO 0118046-A1 15-MAR-2001;
CORIXA CORPORATION (US)

FEATURES Location/Qualifiers
source 1. /organism="Homo sapiens"
misc_feature 1. /note="n = A,T,C or G"
BASE COUNT 129 a 83 c 121 g 62 t 1 others

Query Match 100.0%; Score 21; DB 6; Length 396;
Best Local Similarity 100.0%; Prod. No. 3.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTCTGAGACCGCTCTGGTC 21
Db 145 ATGGTCTGAGACCGCTCTGGTC 125

RESULT 3
BD117323/c
LOCUS 482 bp DNA
DEFINITION EST and encoded human protein.
ACCESSION BD117323
VERSION BD117323.1 GI:23212227
KEYWORDS JUP 2002010789-A/9400
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 482)
AUTHORS Edwards,J.B.D.M., Robert,S. and Giordano,J.E.
TITLE EST and encoded human protein
JOURNAL GENSET CORP
COMMENT OS Homo sapiens (human)
PN JP 2002010789-A/9400
PD 15-JAN-2002
PP 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/114749
PI JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
GIORDANO

FEATURES Location/Qualifiers
source 1. /organism="Homo sapiens"
BASE COUNT 148 a 107 c 150 g 76 t 1 others

Query Match 100.0%; Score 21; DB 6; Length 482;
Best Local Similarity 100.0%; Prod. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTCTGAGACCGCTCTGGTC 21
Db 163 ATGGTCTGAGACCGCTCTGGTC 143

RESULT 4
BD027496/c
LOCUS 491 bp DNA
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD027496
VERSION BD027496.1 GI:22569238
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 491)
AUTHORS Edwards,J.B.D.M., Duclair,B. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
PATENT: JP 2001259182-A 3742 02-OCT-2001;
JOURNAL GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/3742
PD 02-OCT-2001
PP 24-FEB-2000 JP 20000118773
PR 26-FEB-1999 US 60/12487
PI JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCHAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
CC score 6.3
CC seq LLFVGGLLWESG/QV
FH Key
CDS
FT 108. .455
SIg_peptide 108. .455
FEATURES Location/Qualifiers
source 1. /organism="Homo sapiens"
BASE COUNT 149 a 114 c 149 g 78 t 1 others

Query Match 100.0%; Score 21; DB 6; Length 491;
Best Local Similarity 100.0%; Prod. No. 3.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTCTGAGACCGCTCTGGTC 21
Db 194 ATGGTCTGAGACCGCTCTGGTC 174

translation="MKTLLFVGILITWEGQVLDQTSDNELOEMNSGSKYKNE IQNAVNGVQKQIILIEKTNEBKRYARVTCGQGKLGVRQLEPLNOSSEPFYFNGNRGDR ETTMALWECKPCUKIOTCKMFKYARVTCGQGKLGVRQLEPLNOSSEPFYFNGNRGDR LLENDRQTMIDWODHESPRASSILDELEQDRETFEPDDTYHVPESLPHRPFH FKPSRIVRSLMPFSPYEPNLNEFHAFKREMLLSDVSNPNSQAKLRLERDELOVAE RILDKTVCYREIRHNTGCRMKDODCKDLSVQFELMIAQMDLHFSAQFQHPTFIRE SDSDVPSQVLFDFSDPITVVPVTSRNPKFMETAAKQELQERKKKHHRE"	sig_peptide	199.	261.	/note="complement cytolysis inhibitor signal peptide"
	mat_peptide	262.	876	/product="complement cytolysis inhibitor a-chain"
	mat_peptide	877.	1542	/product="complement cytolysis inhibitor b-chain"
BASE COUNT	405	a	481	c
ORIGIN	Unreported.	318	t	9
Query Match	100.0%	Score 21;	DB 9;	Length 1651;
Best Local Similarity	100.0%	Pred. No. 2.9;		
Matches 21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1 ATTTGTCGTGAGACCGTCGTGTC 21			
Db	282 ATTTGTCGTGAGACCGTCGTGTC 262			
RESULT 12	BC019588/c	1658 bp	mRNA	PRI 117-APR-2003
LOCUS	BC019588	Homosapiens clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J), mRNA (cDNA clone MGC:24903 IMAGE:4915444), complete cds.		
DEFINITION				
ORGANISM				
REFERENCE				
AUTHORS				
	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Schuler, G.D., Klausner, R.D., Collins, F.S., Wagner, L., Shemesh, C.M., Schaefer, C.F., Bhat, N.K., Altschuler, S.F., Zeeberg, B., Buetow, K.H., Schaeffer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Diatchenko, L., Matrissina, K., Farmer, A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Tochihiyuki, S., Carninci, P., Prange, C., Raha, S.S., Jaquez, N.A., Peters, G.J., Abramson, R.D., Mullihey, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wark, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulky, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitz, J., Myers, R.M., Butterfield, Y. S., Krzywinski, M.I., Skalska, U., Smallius, D.E., Schnarch, A., Schein, J.E., Jones, S.J. and Marrs, M.A.			
				Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
TITLE				Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL				
MEDLINE				
PUBMED	22383257			
REFERENCE	12477932			
AUTHORS				
TITLE				
JOURNAL				
REMARK				
COMMENT				
				NIH-MCG Project URL: http://mgc.nci.nih.gov
				Contact: MCG help desk

REFERENCE	Mammalia; Eutheria; Primates; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Philippard,D., VasanthaKamur,G., Dotson,S. and Ma,X.J.
TITLE	Osteoarthritis tissue derived nucleic acids, polypeptides, vectors, and cells
JOURNAL	Patent: WO 0153531-A 16 26-JUL-2001; Pharmacia Corporation (US)
FEATURES	Location/Qualifiers
source	1. 1.1678 /organism="Homo sapiens" /mol type="genomic DNA" /db_xref="taxon:9606"
BASE COUNT	424 a 491 c 450 g 313 t
ORIGIN	
Query Match	100.0%; Score 21; DB 6; Length 1678;
Best Local Similarity	100.0%; Pred. No. 2.9;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ATTTGCTGAGACCGCTGGTC 21
Db	156 ATTTGCTGAGACCGCTGGTC 136
RESULT	15
BC010514/c	BC010514 1684 bp mRNA linear PRI 17-APR-2003
LOCUS	Homo sapiens clusterin (Complement lysis inhibitor, SP-40,40, apolipoprotein J), mRNA (cDNA clone MGAC:18080 IMAGE:4150452), complete cds.
DEFINITION	Homo sapiens clusterin (Complement lysis inhibitor, SP-40,40, apolipoprotein J), mRNA (cDNA clone MGAC:18080 IMAGE:4150452), complete cds.
ACCESSION	BC010514.1 GI:14714740
VERSION	MCC.
KEYWORDS	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1684)
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collings,F.S., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A., Rubin,G.M., Stapleton,M., Soares,M.B., Bonaldo,M.F., Usdin,T.B., Tsoi,T., Brownstein,M.J., Casavant,T.L., Carninci,P., Prange,C., Reha,S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mulilahy,S.J., Bosak,S.A., McBewan,P.J., McKernan,K.J., Malek,J., Gunaratna,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Butterfield,Y.S., Krywinski,M.I., Skalska,U., Smailus,D.E., Scheuer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED	12388257
REFERENCE	2 (bases 1 to 1684)
AUTHORS	Strausberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgbms@mail.nih.gov
RESULT	14
AX202086/c	AX202086 Sequence 16 from Patent WO0153531.
LOCUS	1678 bp DNA linear PAT 30-AUG-2001
DEFINITION	Best Local Similarity 100.0%; Pred. No. 2.9;
ACCESSION	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
VERSION	Qy 1 ATTTGCTGAGACCGCTGGTC 21
KEYWORDS	Db 134 ATTTGCTGAGACCGCTGGTC 114
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center Code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lousegd, H.,
 Kovis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IMAK Plate: 19 Row: o Column: 12.

Location/Qualifiers

1.. 1684

/note="Homo sapiens"

/mol type="mRNA"

/db_xref="taxon:9606"

/clone="MGC:18080 IMAGE:4150452"

/tissue type="brain, glioblastoma with EGFR amplification"

/clone lib="NCI CGAP_Bridge4"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

1.. 1684

/note="synonyms: APOU, CLU, SP-40, SGP-2, TRPM-2,
 TRPM2"

/db_xref="MGI:1191"

/db_xref="NM:1854300"

/codon_start=1

/product="clusterin (complement lysis inhibitor, SP-40, 40,
 sulfated glycoprotein 2, testosterone-repressed prostate
 message 2, apolipoprotein J)"

/protein_id="AAH10541"

/db_xref="G:14714741"

/db_xref="MGI:1191"

/translation="MVKTKLIFVGLLTWEGOVLGDOTVSDNELOEMSNQGSKRYVNK
 EIQNAVNGVKQIKLTKTKINERKTLJSNLNEAKKKEDLINEFRESEYKKEELPGVC
 KETQMLAWECKQKPLCKLTKMCFYARCRSGGGLVGRQLBEELNQSPYFWMNEDRID
 SLLENDRQTMVLDYMDHFRASSITDEQDRFTREPODTYHLPSPSLHERPHF
 FFPKSRIVSLMPSPYPLHMPPEFIRHESPAFHPPPEFIRHESPAFHPPPEFIR
 ECGDDDRIVCERHNSTGCLMKDQCDKCRELLSVDCTINNPSQKLRELDLSQVA
 ERILTRKYNELLKSYKOMMLNTSLLBOLNEFNNWYSLRANTGQDQYTLRVTVAASH
 TSDSDVPSGVTEVYVWLFSDPITYVPEVSKPKEFVTAEQLQEVYRKHREE"

BASE COUNT

433 a 493 c 448 g 310 t

ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1684;

Best Local Similarity 100.0%; Prod. No. 2.9; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTGAGACCGCTGTCGC 21

Db 155 ATGGCTGAGACCGCTGTC 135

Search completed: January 21, 2004, 12:11:43

Job time : 807 secs

This Page Blank (uspto)

This clone is available royalty-free through LInL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

Seq Primer: -40UP from Gibco.

FEATURES

source

1. 152
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_Xref="taxon:9606"
 /clone="IMAGE:78594"
 /sex="male"
 /issue_type="frontal lobe"
 /dev_stage="5 months post-conception"
 /lab_host="DIAOB"
 /clone.lib="Schneider fetal brain 00004"
 /note="Organ: brain; Vector: pBluescript SK (Stratagene); Site 1: SstI; Site 2: XbaI; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-GAGAGAGAGCTCAAGGATCTGAGTTTTTTTTTTT-3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Library was constructed by Dr. Claudio Schneider (IINCIB-Area Science Park, Trieste, Italy)."
 BASE COUNT 27 a 43 c 28 g 54 t
 ORIGIN

Query Match 100.0% Score 21; DB 9; Length 152;
 Best Local Similarity 100.0%; Pred. No. 7.;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 KEYWORD 1 ATTGTCTGAGACCGCTGTC 21
 Db 100 ATTGTCTGAGACCGCTGTC 120

RESULT 2
 BF922862/c
 LOCUS QVA-NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 DEFINITION NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF922862
 VERSION 1
 KEYWORD EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

RESULT 2
 BF922862/c
 LOCUS QVA-NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 DEFINITION NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF922862
 VERSION 1
 KEYWORD EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

RESULT 2
 BF922862/c
 LOCUS QVA-NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 DEFINITION NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF922862
 VERSION 1
 KEYWORD EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

RESULT 2
 BF922862/c
 LOCUS QVA-NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 DEFINITION NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF922862
 VERSION 1
 KEYWORD EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

RESULT 2
 BF922862/c
 LOCUS QVA-NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 DEFINITION NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF922862
 VERSION 1
 KEYWORD EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

RESULT 2
 BF922862/c
 LOCUS QVA-NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 DEFINITION NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF922862
 VERSION 1
 KEYWORD EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

RESULT 2
 BF922862/c
 LOCUS QVA-NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 DEFINITION NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF922862
 VERSION 1
 KEYWORD EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

RESULT 2
 BF922862/c
 LOCUS QVA-NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 DEFINITION NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF922862
 VERSION 1
 KEYWORD EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

RESULT 2
 BF922862/c
 LOCUS QVA-NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 DEFINITION NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF922862
 VERSION 1
 KEYWORD EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

RESULT 2
 BF922862/c
 LOCUS QVA-NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 DEFINITION NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF922862
 VERSION 1
 KEYWORD EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

RESULT 2
 BF922862/c
 LOCUS QVA-NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 DEFINITION NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF922862
 VERSION 1
 KEYWORD EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

RESULT 2
 BF922862/c
 LOCUS QVA-NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 DEFINITION NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF922862
 VERSION 1
 KEYWORD EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

RESULT 2
 BF922862/c
 LOCUS QVA-NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 DEFINITION NT0247-201100-262-g12 NT0247 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF922862
 VERSION 1
 KEYWORD EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

(<http://www.ludwig.org.br/scripts/gethtml2.pl?1=QV4&t2=QV4-NT0247-201100-262-g12&t3=2000-11-20&t4=1>)

Seq Primer: puc 18 forward

High Quality sequence start: 15

High Quality sequence stop: 155

Location/Qualifiers

1. 156

/organism="Homo sapiens"

/mol_type="mRNA"

/db_Xref="taxon:9606"

/clone="IMAGE:78594"

/sex="male"

/issue_type="frontal lobe"

/dev_stage="5 months post-conception"

/lab_host="DIAOB"

/clone.lib="Schneider fetal brain 00004"

/note="Organ: brain; Vector: pBluescript SK (Stratagene);

Site 1: SstI; Site 2: XbaI; Double-stranded cDNA was

prepared from human fetal brain tissue. 5' and 3'

adaptors were used in cloning as follows: 5' adaptor

sequence:

5'-GAGAGAGAGCTCAAGGATCTGAGTTTTTTTTT-3'.

The library was

size-selected for >0.5 kb inserts and has an average

insert size estimated at 1.2 kb. This library was

constructed using the CAP-trapper method for full-length

enrichment and has not undergone amplification. Library

was constructed by Dr. Claudio Schneider (IINCIB-Area

Science Park, Trieste, Italy)."

BASE COUNT 27 a 43 c 28 g 54 t

ORIGIN

Query Match 100.0% Score 21; DB 10; Length 156;
 Best Local Similarity 100.0%; Pred. No. 7.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KEYWORD 1 ATTGTCTGAGACCGCTGTC 21

Db 94 ATTGTCTGAGACCGCTGTC 74

RESULT 3
 BF921576/c
 LOCUS NT0179-171100-004-g01 NT0179 Homo sapiens cDNA, mRNA sequence.

DEFINITION NT0179-171100-004-g01 NT0179 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF921576

VERSION 1

EST.

Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 156)

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Cossia, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de oliveira, P.S., Bucher, P., Jongenseel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.P., de Souza, S.J., and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202653

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202653

PUBMED 10737800

COMMENT Laboratory of Cancer Genetics

Laboratory of Cancer Genetics

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

TE.: +55-11-2704922

FAX: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?1=QV4-NT0179-171100-004-g01&t2=2000-11-17&t4=1>)

Seq primer: puc 18 forward

High Quality sequence start: 16

High Quality sequence stop: 161

Location/Qualifiers

1. 161

/organism="Homo sapiens"

/mol_type="mRNA"

/organism="Homo sapiens"

/mol_type="mRNA"

BASE COUNT	27	a	47	c	31	g	60	t
ORIGIN								
Query Match	100.0%		Score 21;	DB 10;	Length 165;			
Best Local Similarity	100.0%		Pred. No. 7.3;			Score 21;	DB 10;	Length 165;
Matches 21;			Indels 0;			Best Local Similarity 100.0%;	Pred. No. 7.3;	
DEFINITION			Mismatches 0;			Matches 21;	Indels 0;	Gaps 0;
SEQUENCE						Best Local Similarity 100.0%;	Mismatches 0;	
ACCESSION	BF929953					Matches 21;	Indels 0;	
VERSION	EST					Indels 0;	Gaps 0;	
KEYWORDS								
SOURCE	Homo sapiens							
ORGANISM	Homo sapiens							
RESEQUENCING								
REFERENCE	1 (bases 1 to 167)							
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldmann, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.P., de Souza, S.J. and Simpson, A.J.							
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed							
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)							
YEAR	2000							
COMMENT	Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil							
FEATURES								
source								
ORGANISM	"Homo sapiens"							
MOL_TYPE	"mRNA"							
DB_XREF	"taxon:9606"							
DEV_STAGE	"Adult"							
CLOSE_LIB	"NT0198"							
NOTE	"Organ: nervous tumor; Vector: puc18; Site: 1: Small; Site: 2: Small; A mini-Library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research, profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."							
BASE COUNT	60	a	48	9	27	t		
ORIGIN								
Query Match	100.0%		Score 21;	DB 10;	Length 167;			
Best Local Similarity	100.0%		Pred. No. 7.4;			Score 21;	DB 10;	Length 167;
Matches 21;			Indels 0;			Best Local Similarity 100.0%;	Pred. No. 7.4;	
DEFINITION			Mismatches 0;			Matches 21;	Indels 0;	Gaps 0;
SEQUENCE								
ACCESSION	1 ATTGCTGAGACCGCTCTGTC 21							
VERSION	EST							
KEYWORDS								
SOURCE	Homo sapiens							
ORGANISM	Homo sapiens							
RESEQUENCING								
REFERENCE	1 (bases 1 to 167)							
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldmann, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.P., de Souza, S.J. and Simpson, A.J.							
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed							
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)							
YEAR	2000							
COMMENT	Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil							
FEATURES								
source								
ORGANISM	"Homo sapiens"							
MOL_TYPE	"mRNA"							
DB_XREF	"taxon:9606"							
DEV_STAGE	"Adult"							
CLOSE_LIB	"NT0198"							
NOTE	"Organ: nervous tumor; Vector: puc18; Site: 1: Small; Site: 2: Small; A mini-Library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research, profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."							
BASE COUNT	60	a	48	9	27	t		

COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=PM1&t2=PM1-NN1200-281100-033-E03&t3=2000-11-28&t4=1>)
 Seq. primer: puc 18 forward
 High quality sequence stop: 177.
 FEATURES
 source
 1.
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NN1105"
 /note="Organ: nervous normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT
 ORIGIN
 Query Match 100.0% Score 21; DB 10; Length 177;
 Best Local Similarity 100.0% Pred. No. 7.5; Mismatches 0; Gaps 0;
 Matches 21; Conservative 0; Indels 0; Gaps 0;
 QY 1 ATTGTCTGAGACCGTCTGGTC 21
 Db 68 ATTGTCTGAGACCGTCTGGTC 48
 RESULT 10
 BL036860/c
 LOCUS MR4-NT0140-080101-209-c09 NT0140 Homo sapiens cDNA, mRNA sequence.
 DEFINITION EST
 ACCESSION BI036860
 VERSION BI036860.1 GI:14443486
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; 1 (bases 1 to 185)
 REFERENCE Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 AUTHORS Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J., and
 Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBLMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=PM1&t2=PM1-NN1200-281100-033-E03&t3=2001-01-08&t4=1>)
 Seq. primer: puc 18 forward
 High quality sequence start: 17
 High quality sequence stop: 134.
 FEATURES
 source
 1.
 /organism="Homo sapiens"
 /mol_type="mRNA"

/db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NT0140"
 /note="Organ: nervous tumor; Vector: pUC18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 Profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 41 a 42 c 62 g 40 t
 ORIGIN

Query Match 100.0% Score 21; DB 12; Length 185;
 Best Local Similarity 100.0% Pred. No. 7.6; 0: Indels 0: Gaps 0;
 Matches 21; Conservative 0; Mismatches 0;
 Qy 1 ATGGCTGAGACCGTCTGTC 21
 Db 109 ATGGCTGAGACCGTCTGTC 89

RESULT 11
 LOCUS BI037432 190 bp mRNA linear EST 14-JUN-2001
 DEFINITION CM-NT0067-110101-588-h12 NT0267 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BI037432
 VERSION BI037432.1 GI:14444058
 KEYWORD EST
 SOURCE Homo sapiens (human)
 ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 190)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.P., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and
 Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?1=CM3&t2=CM3-NT0267-110101-588-h12&t3=201-01-11&t4=1>)
 Seq primer: Puc 18 forward
 High quality sequence stop: 193.
 Location/Qualifiers
 1. 1-193
 .organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NT0267"
 /note="Organ: nervous tumor; Vector: pUC18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 Profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 70 a 39 c 57 g 27 t
 ORIGIN

Query Match 100.0% Score 21; DB 10; Length 193;
 Best Local Similarity 100.0% Pred. No. 7.8; 0: Indels 0: Gaps 0;
 Matches 21; Conservative 0; Mismatches 0;
 Qy 1 ATGGCTGAGACCGTCTGTC 21

Db 72 ATTGCTGAGACCGTCGGTC 52

RESULT 13
 AT745406 LOCUS AT745406 DEFINITION wc3\do1.xt1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2320801_3, similar to gb: X14723 CLUSTERIN PRECURSOR (HUMAN); mRNA sequence.

ACCESSION AT745406 VERSION AT745406_1 KEYWORD Homo sapiens (human)

ORGANISM Homo sapiens Mammalia: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominoidea; Homo. (bases 1 to 201)

REFERENCE AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Goldmann, G.H., Carvalho A.F., Matsukuma, A., Bajaj, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, P., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 200202653 PUBLMED 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: a Simpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethm12.pl?t1=PM1&t2=PM1-NN1200-251100-007-c09&t3=2000-11-25&t4=1)

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI- CGAP clone distribution information can be found through the T.M.A.G.E. Consortium/NN11 at: www-bio.llnl.gov/bbrp/IMAGE/image.html

Insert Length: 264 Std Error: 0.00

Seq primer: -40UP from Gibco.

FEATURES Source

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgsapbs r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmett-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI- CGAP clone distribution information can be found through the T.M.A.G.E. Consortium/NN11 at: www-bio.llnl.gov/bbrp/IMAGE/image.html

Insert Length: 264 Std Error: 0.00

Seq primer: -40UP from Gibco.

FEATURES Location/Qualifiers

1. 196 /organism="Homo sapiens"
 /mol type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2320801"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI-CGAP Pr28"
 /note="Organ: Prostate; Vector: PT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI-CGAP Pr22 was prepared, and 55 circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR amplified cDNAs from a pool of 5,000 clones made from the same library (clone IDs 985608-986759, 1101192-1101959, and 1217328-1220615).
 39 a 60 c 35 g 62 t

BASE COUNT ORIGIN

RESULT 14
 Query Match 100.0% Score 21; DB 9; Length 196;
 Best Local Similarity 100.0% Pred. No. 7.8; Matches 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0; Indels 0;

DEFINITION PM1-NN1200-271100-008-a07 NN1200 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF957858
 VERSION BF957858-1
 KEYWORDS EST.

ORGANISM Homo sapiens (human)

REFERENCE AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Goldmann, G.H., Carvalho A.F., Matsukuma, A., Bajaj, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, P., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, São Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/geshtm12.p?t1=PM1&t2=PM1-NN1200-27100-008-a07&t3=2000-11-27&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 24
 High quality sequence stop: 182.
 FEATURES Location/Qualifiers
 1. 207
 source
 /organism="Homo sapiens"
 /mol type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone lib="NN1200"
 /note="Organ: nervous normal; Vector: puc18; site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT
 ORIGIN 51 a 45 c 71 g 40 t
 Query Match 100.0%; Score 21; DB 10; Length 207;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGGCTGAGCCCTCTGTC 21
 Db 143 ATTCCTGGACCCCTCTGTC 123
 Search completed: January 21, 2004, 13:09:41
 Job time : 1738 secs

XX Claim 4; Page 36; 38pp; English.
 PS The present sequence is an antisense oligonucleotide directed at the human testosterone-repressed prostate message-2 (TRPM-2, also known as clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to promote the regression of tumours, and oligonucleotides directed at the TRPM-2 gene, can be used in the treatment of tumour cells expressing some breast cancer cells. In addition to this, they also increase the chemosensitivity of the cells, meaning that conventional chemotherapy is more effective.
 XX Sequence 21 BP; 3 A; 5 C; 6 G; 7 T; 0 other;
 XX Query Match 100.0%; Score 21; DB 21; Length 21;
 XX Best Local Similarity 100.0%; Pred. No. 0.25;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGCTGAGACCCGCTCTGGTC 21
 DB 1 ATTGCTGAGACCCGCTCTGGTC 21

QY 1 ATTGCTGAGACCCGCTCTGGTC 21

DB 1 ATTGCTGAGACCCGCTCTGGTC 21

QY 1 ATTGCTGAGACCCGCTCTGGTC 21

DB 1 ATTGCTGAGACCCGCTCTGGTC 21

QY 1 ATTGCTGAGACCCGCTCTGGTC 21

DB 1 ATTGCTGAGACCCGCTCTGGTC 21

QY 1 ATTGCTGAGACCCGCTCTGGTC 21

DB 1 ATTGCTGAGACCCGCTCTGGTC 21

QY 1 ATTGCTGAGACCCGCTCTGGTC 21

DB 1 ATTGCTGAGACCCGCTCTGGTC 21

QY 1 ATTGCTGAGACCCGCTCTGGTC 21

DB 1 ATTGCTGAGACCCGCTCTGGTC 21

QY 1 ATTGCTGAGACCCGCTCTGGTC 21

DB 1 ATTGCTGAGACCCGCTCTGGTC 21

QY 1 ATTGCTGAGACCCGCTCTGGTC 21

DB 1 ATTGCTGAGACCCGCTCTGGTC 21

QY 1 ATTGCTGAGACCCGCTCTGGTC 21

DB 1 ATTGCTGAGACCCGCTCTGGTC 21

QY 1 ATTGCTGAGACCCGCTCTGGTC 21

DB 1 ATTGCTGAGACCCGCTCTGGTC 21

QY 1 ATTGCTGAGACCCGCTCTGGTC 21

DB 1 ATTGCTGAGACCCGCTCTGGTC 21

QY 1 ATTGCTGAGACCCGCTCTGGTC 21

DB 1 ATTGCTGAGACCCGCTCTGGTC 21

QY 1 ATTGCTGAGACCCGCTCTGGTC 21

DB 1 ATTGCTGAGACCCGCTCTGGTC 21

QY 1 ATTGCTGAGACCCGCTCTGGTC 21

DB 1 ATTGCTGAGACCCGCTCTGGTC 21

QY 1 ATTGCTGAGACCCGCTCTGGTC 21

DB 1 ATTGCTGAGACCCGCTCTGGTC 21

QY 1 ATTGCTGAGACCCGCTCTGGTC 21

DB 1 ATTGCTGAGACCCGCTCTGGTC 21

QY 1 ATTGCTGAGACCCGCTCTGGTC 21

DB 1 ATTGCTGAGACCCGCTCTGGTC 21

CC be used to inhibit the function of genes associated with sensitivity to PDS. For enhancement of chemotherapy, a GSE can be transferred (either alone or with another gene) on an expression vector into blood progenitor cells from a cancer patient. The cells are returned to the patients circulation, and allowed to repopulate the blood before aggressive chemotherapy is carried out (using higher cisplatin concentrations than normal), this will thereby avoid toxic side effects to the immune system as the blood cells will be GSE resistant.

XX SQ Sequence 195 BP; 46 A; 45 C; 71 G; 33 T; 0 other;
 XX Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Query Match 100.0%; Score 21; DB 16; Length 195;
 XX Best Local Similarity 100.0%; Pred. No. 0.37;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 ABT03091/C
 ID ABT03091 standard; cDNA; 396 BP.
 XX
 AC ABL4874;
 XX
 DT 05-SEP-2002 (first entry)
 XX
 DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 15.
 XX
 KW ovarian cancer; ovarian carcinoma; gene therapy; immunotherapy;
 KW cytostatic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200239885-A2.
 XX
 PD 23-MAY-2002.
 XX
 PP 13-NOV-2001; 2001WO-US45395.
 XX
 PR 14-NOV-2000; 2000US-0713550.
 PR 03-APR-2001; 2001US-0825294.
 PR 02-OCT-2001; 2001US-0970966.
 PA (CORI-X CORP.
 PR
 PI Xu J, Stolk JA, Algata PA, Fling SP, Moleshi DA;
 DR WPI; 2002-500186/53.
 PR
 Novel ovarian cancer polypeptide and polynucleotide, useful for
 detecting the presence of ovarian cancer in a patient, and in
 pharmaceutical compositions, e.g. vaccines, for treating ovarian cancer
 PR
 Example 1; Page 117; 197pp; English.
 XX
 CC The present invention provides human ovarian cancer associated proteins
 CC and coding sequences. The sequences can be used in the diagnosis and
 CC treatment of ovarian cancers. The present sequence is a coding sequence
 CC of the invention.
 XX
 SQ Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 1 other;
 SQ Query Match 100.0%; Score 21; DB 24; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATTGGCTGAGACCGCTGGTC 21
 Db 145 ATTGGCTGAGACCGCTGGTC 125

RESULT 5
 ABL4874/C
 ID ABL4874 standard; cDNA; 396 BP.
 XX
 AC ABL4874;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Ovarian carcinoma sequence isolate 23657-1.
 XX
 KW Ovarian cancer; cancer therapy; vaccine; gene therapy; tumour; cancer;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PN US2002004491-A1.
 XX
 PD 10-JAN-2002.

XX
 03-APR-2001; 2001US-0825294.
 XX
 PF 10-SEP-1999; 99US-0394374.
 PR 01-MAY-2000; 2000US-061778.
 PR 15-AUG-2000; 2000US-0640173.
 PR 07-SEP-2000; 2000US-0656668.
 PR 14-NOV-2000; 2000US-0713550.
 XX
 PA (XU J/) XU J.
 PA (STOLK/) STOLK J A.
 PA (ALGATE/) ALGATE P A.
 PA (FLING/) FLING S P.
 XX
 PI Xu J, Stolk JA, Algata PA, Fling SP;
 XX
 DR WPI; 2002-171027/22.
 XX
 PT Ovarian tumour polypeptide and polynucleotide useful in diagnosis,
 PR prevention and/or treatment of cancer, especially ovarian cancer.
 XX
 PS Example 1; Page 43; 131pp; English.
 XX
 CC The invention relates to ovarian tumour polypeptides and polynucleotides
 CC that may be utilised in cancer therapy, for example in a vaccine or
 CC gene therapy. Polypeptides and polynucleotides of the invention are
 CC useful for detecting a cancer in a patient, for stimulating and/or
 CC expanding T-cells specific for a tumour protein, and for inhibiting the
 CC development of a cancer in a patient. They are also useful for
 CC stimulating an immune response in a patient, and for treating a cancer in
 CC a patient and for determining the presence of a cancer in a patient.
 CC The isolated polynucleotides of the invention are useful for their
 CC ability to selectively form duplex molecules with complementary stretches
 CC of the entire desired gene or gene fragments, and for designing and
 CC preparing ribozyme molecules for inhibiting expression of tumour
 CC polypeptides in tumour cells. Polypeptides and polynucleotides of the
 CC invention are also useful in recombinant DNA molecules to direct
 CC expression of a polypeptide in appropriate host cells. The sequences
 CC given in records ABL4874-0-BL48956 represent polynucleotides encoding
 CC ovarian carcinoma Proteins.
 XX
 SQ Sequence 396 BP; 129 A; 83 C; 121 G; 62 T; 1 other;
 SQ Query Match 100.0%; Score 21; DB 24; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATTGGCTGAGACCGCTGGTC 21
 Db 145 ATTGGCTGAGACCGCTGGTC 125

RESULT 6
 AAC03751/C
 ID AAC03751 standard; cDNA; 491 BP.
 XX
 AAC03751;
 AC
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 3749.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW Gene therapy; chromosome mapping; ss.
 XX
 CS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PP 21-FEB-2000; 2000EP-02000610.

PR 26-FEB-1999; 99US-0122487.
 XX (GEST) GENSET.
 PA
 PI Dumas Milne Edwards J., Duclert A., Giordano J.;
 XX WPI; 2000-50381/45.
 DR P-PSDB; ARG03745.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for diagnostic, forensic, gene therapy and chromosome mapping procedures -
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT
 PS Claim 1; SEQ ID 3749; 71pp + CD-ROM; English.
 CC The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
 XX SQ Sequence 491 BP; 149 A; 114 C; 149 G; 78 T; 1 other;
 Query Match 100.0%; Score 21; DB 21; Length 491;
 Best Local Similarity 100.0%; Prod. No. 0.43; ID AAZ42136 standard; cDNA: 572 BP.
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATTTGCTGAGACCCCTCTGGTC 21
 Db 194 ATTTGCTGAGACCCGTC 174
 XX
 RESULT 7
 AAU89150/C
 ID AAU89150 standard; cDNA; 512 BP.
 AC
 XX DE 15-FEB-1999 (first entry)
 EST clone CG1.
 XX Human; secreted protein; expressed sequence tag; EST; haematopoiesis 1
 KW tissue growth; chemotaxis; haemostatic; haemostatic;
 KW receptor; ligand; thrombolytic; anti-inflammatory;
 KW gene therapy; ss.
 OS Homo sapiens.
 XX PN WO9845436-A2.
 XX PD 15-OCT-1998.
 XX PF 10-APR-1998; 98WO-US06955.
 XX PR 10-APR-1997; 97US-0838821.
 PA (GEMI) GENETICS INST INC.
 XX AGOSTINO MJ, Jacobs K, Lavallie ER, MCCOY JM, Merberg D;
 PI Racie LA, Spaulding V, Tracy M;
 XX WPI; 1999-070077/06.
 XX
 PT New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.
 XX
 PS Claim 1; Page 126; 618pp; English.
 CC The present sequence represents a human expressed sequence tag (EST).
 CC The polynucleotide, which is a secreted EST, and the encoded protein
 CC are predicted to have useful biological activities which would make
 CC them suitable for treating, preventing or ameliorating medical
 CC conditions in humans and animals although no supporting data is
 CC given. Suggested activities include nutritional activity, immune
 CC stimulating or suppressing activity, antiviral/inhibin activity,
 CC activity, tissue growth activity, activin/inhibin activity,
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
 CC activity, receptor/ligand activity, anti-inflammatory activity,
 CC cadherin/tumour invasion suppressor activity, tumour inhibitory
 CC activity. The polynucleotide may also be useful for gene therapy.
 XX SQ Sequence 512 BP; 154 A; 114 C; 150 G; 94 T; 0 other;
 Query Match 100.0%; Score 21; DB 20;
 Best Local Similarity 100.0%; Prod. No. 0.43;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATTTGCTGAGACCCGTC 21
 Db 121 ATTTGCTGAGACCCGTC 101
 XX
 RESULT 8
 AAZ42136/C
 ID AAZ42136 standard; cDNA: 572 BP.
 XX AC AAZ42136;
 XX DT 31-JAN-2000 (first entry)
 XX DS Human normal bladder tissue cDNA derived EST 15.
 XX KW Human; bladder; treatment; EST; expressed sequence tag; cytostatic;
 KW cancer; gene therapy; ss.
 XX OS Homo sapiens.
 XX PN DB19818620-A1.
 XX PD 28-OCT-1999.
 XX PF 21-APR-1998; 98DE-1018620.
 XX PR 21-APR-1998; 98DE-1018620.
 XX PA (META-) METAGEN GES GENOMFORSCHUNG NBH.
 XX PT New polypeptides and their nucleic acids, useful for treatment of
 PT bladder tumour and identification of therapeutic agents -
 XX
 PS Claim 3; Page 158; 366pp; German.
 XX
 CC This invention describes novel polypeptide fragment sequences (I) and
 CC their encoding nucleic acids (II) which are highly expressed in normal
 CC bladder tissue and have cytostatic activity. (II) are used for
 CC recombinant expression of (I) and to isolate complete genes. (I) are
 CC used to identify agents suitable for the treatment of bladder tumours,
 CC to directly treat this form of cancer (including expression from gene
 CC therapy vectors), or are used in a preparation for cancer treatment. (II) are
 CC also used for the generation of specific antibodies. (II) are
 CC identified by assembling ESTs (expressed sequence tags) from a

particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, and therefore reduces the number of failures because of ESRs from different libraries representing different parts of the same unknown gene and distorting the estimated frequency of occurrence in a particular tissue.

AR4212-24248 represent EST fragments derived from a human normal bladder tissue cDNA library which encode the protein fragments

Sequence 572 BP; 161 A; 128 C; 186 G; 97 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 572;

Best Local Similarity 100.0%; Pred. No. 0.44; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTCAGACGCTCGGTC 21

DB 262 ATGGTCAGACGCTCGGTC 242

RESULT 9
AB056105/c
ID AB056105 standard; cDNA; 704 BP.

XX AC AB056105;
XX DT 22-AUG-2002 (first entry)

DE Human ovarian antigen HSPH41 cDNA, SEQ ID NO:1985.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; KW KW inflammatory condition; immune disorder; blood disorder; infection; KW KW cardiovascular disorder; respiratory disorder; neurological disorder; KW KW gastrointestinal disorder; urinary system disorder; drug screening; KW KW gene therapy; chromosomal mapping; forensic analysis; KW KW antibody preparation; cytostatic; immunomodulatory; neuroprotective; KW KW antiinflammatory; gynaecological; reproductive; gene; ss.

OS Homo sapiens.

XX WO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US18569.

PR 07-JUN-2000; 2000US-209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX WPI; 2002-147878/19.

DR P-PSDB; ABP43028.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides, prevent in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer, immune disorders, cardiovascular disorders and neurological diseases -

XX PS Claim 1; SEQ ID No 1985; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ5131-ABQ5605), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosis or preventing various ovary and/or breast-related

CC disorders. Such conditions include ovarian cancer and breast cancer, and CC metastatic tumours of ovarian or breast origin, reproductive system CC disorders (e.g., infertility, disorders of pregnancy, anovulation, CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis), and toxic CC shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and CC vaginitis), immune disorders (e.g., autoimmune, systemic lupus erythematosus), CC immunodeficiencies, autoimmune disorders, cardiovascular disorders, CC blood-related disorders, neurological disorders, gastrointestinal disorders, CC respiratory disorders, neurological disorders, polygoptenides and CC and urinary system disorders. Ovarian antigen polygoptenides and CC polynucleotides may also be used in screening for compounds which CC modulate ovarian antigen expression or activity. The polynucleotides may CC be used for gene therapy, chromosome mapping, in the CC identification of individuals and in forensic analysis, and the CC polypeptides may be used as food additives or to prepare antibodies CC useful in disease diagnosis, drug targeting and phenotyping. The present CC sequence represents cDNA, encoding human ovarian antigen of the CC invention.

CC Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 704 BP; 180 A; 197 C; 199 G; 121 T; 7 other;

XX Query Match 100.0%; Score 21; DB 24; Length 704;

XX Best Local Similarity 100.0%; Pred. No. 0.46; Matches 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 ATGGCTGAGACGGCTGGTC 21

XX Db 215 ATGGCTGAGACGGCTGGTC 195

RESULT 10
AAA41857/C
ID AAA41857 standard; cDNA; 922 BP.

XX XX AAA41857;
XX AC AAA41857;
XX DT 21-AUG-2000 (first entry)

XX DE Human secreted expressed sequence tag SEQ ID NO:432.

XX Human; mouse; chicken; rat; secreted expressed sequence tag; sEST;

XX KW expressed sequence tag; EST; probe; chemotactic; proliferative;

XX KW immunomodulatory; haemopoietic; chemokinetic; analgesic; haemostatic;

XX KW thrombolytic; antiinflammatory; cytostatic; antitubercular;

XX KW antiviral; antidiabetic; antiasthmatic; pulmonary; antiparkinsonian;

XX KW ant ulcer; otopathic; neuroprotective; nootropic; antiporiatic;

XX KW cerebroprotective; anticonvulsant; antidepressant; gene therapy;

XX KW vaccine; autoimmune disorder; multiple sclerosis; allergic condition;

XX KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;

XX KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;

XX KW central nervous system disorder; Alzheimer's disease; stroke;

XX KW Parkinson's disease; Huntington's disease; coagulation disorder;

XX KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease;

XX KW tumour; infection; depression; psoriasis; ss.

XX Homo sapiens.

XX WO20021991-A1.

XX PN 20020021991-A1.

XX PD 20-APR-2000.

XX PR 15-OCT-1999;

XX XX 99WO-US24206.

XX PR 15-OCT-1998;

XX XX 98US-0104436.

XX PA (GEMY) GENETICS INST INC.

XX PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;

PI Merberg D, Treacy M, Bowman MR;

XX WPI; 2000-317938/27.
 XX Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTs), useful for treating various disorders -
 XX Claim 1; Page 316; 803pp; English.
 XX AAA45926 to AAA45925 represent specifically claimed secreted expressed sequence tags (SESTs), isolated from human, mouse, chicken and rat tissue sources. The SESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemokinetic; proliferative; immunomodulatory; haemopoietic; chemokine; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; analgesic; osteoprotective; neuroprotective; nootropic; antiparkinsonian; antipsoratic; cerebroprotective; anticonvulsant; and antidepressant. The SESTs can be used for gene therapy and in vaccines. The SESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the SESTs. Proteins encoded by the SESTs are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, spondarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's, disease, stroke), coagulation disorders (haemophilia, thrombophilia), inflammatory disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. AA45926 to AA45931 represent linker variants which are given in the exemplification of the present invention.

XX Sequence 922 BP; 243 A; 265 C; 244 G; 166 T; 4 other;

Query Match 100.0%; Score 21; DB 21; Length 922;
 Best Local Similarity 100.0%; Pred. No. 0.48; Matches 0; Indels 0; Gaps 0;

Qy 1 ATTCGCTGAGACCGCTCTGGTC 21
 Db 118 ATTCGCTGAGACCGCTCTGGTC 98

RESULT 11
 ABZ03527C
 ID ABZ03527 standard; cDNA; 1024 BP.
 XX AC ABZ03527;
 XX DT 14-MAY-2003 (first entry)

DE Toxicologically relevant human nucleotide sequence #686.
 XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haemopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen; ss.

XX WO2003016500-A2.
 PD 27-FEB-2003.
 XX PR 16-AUG-2002; 2002WO-US26514.
 XX PR 16-AUG-2001; 2001US-313080P.

XX PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 XX PI Neft RE; Dunn RT; Adkins K; Pickett GG; Kier LD; Schmeiser K;
 PI Allen P;
 DR WPI; 2003-268322/26.
 XX PD 13-SEP-2001.
 XX PF 05-MAR-2001; 2001WO-US04942.
 XX PR 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0536193.
 XX

PT Determining a toxicological response to an agent, useful for screening of drugs, comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of toxicity -
 PT XX
 PS XX
 PS Claim 1; Page 232; 455pp; English.

CC The present invention describes a method (M1) for determining a toxicological response to an agent, which comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of toxicity, and so determining the presence of a toxic response to the agent. Also described: (1) an array comprising one or more polynucleotides selected from the genes corresponding to the partial sequences given in ABZ02842 to ABZ04764, or their fragments of at least 20 nucleotides, or homologues; and (2) determining if a gene putatively identified to be a toxic response gene plays a role on toxic response pathways by determining the expression profile of the gene after exposure of cells or a human subject to a known toxic pharmaceutical or industrial agent, comprising: (a) exposing cells to an agent or isolating cells from a human subject who was exposed to an agent; (b) obtaining the test gene expression profile for a putatively identified toxic response gene after exposure to a known toxic pharmaceutical or industrial agent; and (c) comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of that gene after exposure to other known toxic compounds. The methods are useful for predicting and determining toxicological responses on a cellular, organ or system level. The arrays comprising the human genes are useful for toxicological screening of drugs, pharmaceutical compounds and chemicals.

XX Sequence 1024 BP; 262 A; 299 C; 278 G; 185 T; 0 other;

Query Match 100.0%; Score 21; DB 25; Length 1024;
 Best Local Similarity 100.0%; Pred. No. 0.49;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATTCGCTGAGACCGCTCTGGTC 21
 Db 134 ATTCGCTGAGACCGCTCTGGTC 114

RESULT 12

AAS44948/C
 ID AAS44948 standard; cDNA; 1568 BP.
 XX AC AAS44948;

XX DT 18-DEC-2001 (first entry)
 XX DE CDNA encoding novel human secretory protein, Seq ID No 29.
 XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haemopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen; ss.

XX Homo sapiens.
 XX OS WO200166689-A2.
 XX PN WO200166689-A2.

XX PD 13-SEP-2001.
 XX PF 05-MAR-2001; 2001WO-US04942.

XX PR 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0536193.
 XX

PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0665363.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 (HYSEQ) HYSEQ INC.
 XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P; PI Zhao QH, Yang Y, Dumanac RT, Zhang J, Chen R, Xue AJ, Wang J; XX DR; WPI; 2001-589934/66.
 DR -PSDB; AAU28048.
 XX
 PR Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of PR cancer, neurological, inflammatory, and autoimmune disorders -
 XX
 PS Claim 1; SEQ ID No 29; 107pp; English.
 XX
 CC The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haemopoiesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis. In addition, (I) is involved in hematocytic or chemokinetic activity, regulation of haemopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, CC reperfusion injury in various tissues, various immune deficiencies and CC disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, CC rheumatoid arthritis, diabetic mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. CC In addition, (I) affects biorhythms or circadian cycles of rhythms, CC fertility, metabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an CC immune response. AAS41920-AAS45295 represent novel human secreted protein CC coding sequences of the invention.
 XX
 SQ Sequence 1568 BP; 386 A; 456 C; 434 G; 292 T; 0 other;
 Query Match 100.0%; Score 21; DB 22; Length 1568;
 Best Local Similarity 100.0%; Pred. No. 0.52%;
 Matches 21; Conservatory 0; Indels 0; Gaps 0;
 YY 1 ATTGTCCTGAGACCGTCTGGTC 21
 Db 156 ATTGTCCTGAGACCCGCTGGTC 136
 RESULT 13
 ABS78654.C
 ID ABS78654 standard; CDNA; 1589 BP.
 XX
 AC ABS78654;
 XX
 DT 16-DEC-2002 (first entry)
 XX DE Human cDNA encoding CGDD12, INCYTE 7503618CB1.
 XX

SQ Sequence 1589 BP; 407 A; 421 C; 466 G; 295 T; 0 other;
 Query Match 100.0%; Score 21; DB 24; Length 1589;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 KW cytolysis inhibitor; perforin; immunological effector molecule;
 DE Cytolysis Inhibitor gene.
 Qy 1 ATTGTCTGAGACCGTCTGGTC 21
 Db 164 ATTGTCTGAGACCGTCTGGTC 144
 OS Homo sapiens.
 XX
 RESULT 14
 ABN9656/C
 ID ABN9656 standard; DNA; 1648 BP.
 XX
 AC ABN9656;
 XX
 DT 16-AUG-2002 (first entry)
 XX
 DE Human clusterin gene sequence 1.
 XX
 KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
 KW hypercholesterolemia; cardiovascular disorder; ds;
 KW hyperproliferative disorder; hyperlipidemic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO20022635-A1.
 XX
 PD 21-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US28235.
 XX
 PR 11-SEP-2000; 2000US-0659791.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Friier SM;
 XX
 WPI: 2002-404805/43.
 DR -PDB: AAO15039.
 XX
 Novel antisense compound targeted to nucleic acid molecule encoding
 clusterin, useful for treating animal having disease associated with
 clusterin such as hyperlipidemic disorder, cardiovascular disorder -
 XX
 PS Example 13; Page 89-92; 125bp; English.
 XX
 The invention comprises antisense oligonucleotides that are capable of
 inhibiting expression of the human clusterin gene. The antisense
 oligonucleotides of the invention are useful for inhibiting the
 expression of clusterin in cells. The antisense oligonucleotides are also
 useful for treating an animal with a disease or condition associated with
 clusterin (e.g. hypercholesterolemia; cardiovascular disorders;
 hyperproliferative disorders; and hyperlipidemic disorders). The present
 DNA sequence represents a human clusterin gene sequence.
 XX
 Sequence 1648 BP; 408 A; 488 C; 440 G; 312 T; 0 other;
 CC The invention comprises antisense oligonucleotides that are capable of
 inhibiting expression of the human clusterin gene. The antisense
 oligonucleotides of the invention are useful for inhibiting the
 expression of clusterin in cells. The antisense oligonucleotides are also
 useful for treating an animal with a disease or condition associated with
 clusterin (e.g. hypercholesterolemia; cardiovascular disorders;
 hyperproliferative disorders; and hyperlipidemic disorders). The present
 DNA sequence represents a human clusterin gene sequence.
 XX
 Query Match 100.0%; Score 21; DB 24; Length 1648;
 Best Local Similarity 100.0%; Pred. No. 0.53;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 KW infectivity; ss.
 DE
 Qy 1 ATTGTCTGAGACCGTCTGGTC 21
 Db 139 ATTGTCTGAGACCGTCTGGTC 119
 OS Homo sapiens.
 XX
 Key FH
 sig_peptide 199..261
 FT /*tag= a
 mat_peptide 262..1542
 FT /*tag= b
 /product= cytolysis inhibitor
 XX
 DE3933850-A.
 XX
 PD 18-APR-1991.
 XX
 KW 06-OCT-1999; 89DE-3933850.
 XX
 PR 06-OCT-1999; 89DE-3933850.
 XX
 PA (SCHD) SCHERING AG.
 XX
 PI Tschoopp J, Jenne D;
 DR WPI; 1991-118338/17.
 XX
 PT DNA sequence coding for cytolysis inhibitor - is strong inhibitor
 of terminal complement protein, e.g. perforin secreted by killer
 cells
 XX
 PS Claim 2; Page 8; 15pp; German.
 XX
 Two probes were prepared based on the known partial amino acid
 sequences of both chains of the Cytolysis Inhibitor and used to
 screen a liver-specific cDNA library. One clone which hybridised
 positively to both probes was found to contain a 1.7kb BamHI-³PNI
 fragment. This was inserted into plasmid PGEM4, to give EGEM4/21-1.
 CC E.coli transformed with the plasmid are deposited under DSM # 52659.
 CC The insert has the sequence given in this file.
 CC See also AAO1501 and AAO1502.
 XX
 SQ Sequence 1651 BP; 405 A; 481 C; 447 G; 318 T; 0 other;
 CC Query Match 100.0%; Score 21; DB 12; Length 1651;
 CC Best Local Similarity 100.0%; Pred. No. 0.53;
 CC Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATTGTCTGAGACCGTCTGGTC 21
 Db 282 ATTGTCTGAGACCGTCTGGTC 262
 OS Homo sapiens.
 XX
 Search completed: January 21, 2004, 11:44:45
 Job time : 151 secs

RESULT 15
 AAO1503/C
 ID AAO1503 standard; DNA; 1651 BP.
 XX
 AC AAO1503;

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: January 21, 2004, 12:11:53 : Search time 217 Seconds
 (without alignments)

341.106 Million cell updates/sec

Title: US-09-913-325-5

Perfect score: 21

Sequence: 1 atgttgtagaccgtctggtc 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2324096 seqs, 162381658 residues

Total number of hits satisfying chosen parameters: 4648192

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database :

Published_Applications_NA.*

1: /cn2_6_ptodata/2/pubna/us07_PUBCOMB.seq/*
 2: /cn2_6_ptodata/2/pubna/US07_PUBCOMB.seq/*
 3: /cn2_6_ptodata/2/pubna/US06_NEW_PUB.seq/*
 4: /cn2_6_ptodata/2/pubna/US06_PUBCOMB.seq/*
 5: /cn2_6_ptodata/2/pubna/us07_NEW_PUB.seq/*
 6: /cn2_6_ptodata/2/pubna/pcus2_PUBCOMB.seq/*
 7: /cn2_6_ptodata/2/pubna/us08_NEW_PUB.seq/*
 8: /cn2_6_ptodata/2/pubna/us08_PUBCOMB.seq/*
 9: /cn2_6_ptodata/2/pubna/us09A_PUBCOMB.seq/*
 10: /cgn2_6_ptodata/2/pubna/us09B_PUBCOMB.seq/*
 11: /cgn2_6_ptodata/2/pubna/us09C_PUBCOMB.seq/*
 12: /cgn2_6_ptodata/2/pubna/us09_NEW_PUB.seq/*
 13: /cgn2_6_ptodata/2/pubna/us10A_NEW_PUB.seq/*
 14: /cgn2_6_ptodata/2/pubna/us10B_PUBCOMB.seq/*
 15: /cgn2_6_ptodata/2/pubna/us10C_PUBCOMB.seq/*
 16: /cgn2_6_ptodata/2/pubna/us10_NEW_PUB.seq/*
 17: /cgn2_6_ptodata/2/pubna/us60_NEW_PUB.seq/*
 18: /cgn2_6_ptodata/2/pubna/us60_PUBCOMB.seq/*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
 US-09-944-326-5
 Sequence 5, Application US/09944326
 Patent No. US20020128220A1

GENERAL INFORMATION:
 / APPLICANT: Gleave, Martin S.
 / APPLICANT: Remnie, Paul S.
 / APPLICANT: Miyake, Hideaki
 / APPLICANT: Nelson, Colleen
 / APPLICANT: Rennie, Paul S.
 / TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
 / FILE REFERENCE: UBC_P-020-2
 / CURRENT APPLICATION NUMBER: US/09/944_326
 / CURRENT FILING DATE: 2001-08-30
 / PRIOR APPLICATION NUMBER: 60/121,726
 / PRIOR FILING DATE: 1999-02-26
 / PRIOR APPLICATION NUMBER: 09/913_325
 / PRIOR FILING DATE: 2001-08-10
 / NUMBER OF SEQ ID NOS: 14
 / SOFTWARE: Patentin Ver. 2.1
 / SEQ ID NO: 5
 / LENGTH: 21
 / ORGANISM: HUMAN
 / FEATURE:
 / OTHER INFORMATION: antisense TRPM-2 CDN

US-09-944-326-5
 Query Match 100.0%; Score 21; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.57%;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTGTCTGAGACCGTGTGGTC 21
 Db 1 ATTGTCTGAGACCGTGTGGTC 21

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	21	100.0	21	10	US-09-944_326-5	Sequence 5, Appli
2	21	100.0	21	13	US-09-944_326-5	Sequence 5, Appli
3	21	100.0	21	13	US-10-080-794-5	Sequence 5, Appli
c 4	21	100.0	195	12	US-10-404-579-14	Sequence 14, Appli
c 5	21	100.0	396	9	US-09-825-294-15	Sequence 15, Appli
c 6	21	100.0	396	10	US-09-970-966-15	Sequence 15, Appli
c 7	21	100.0	396	12	US-10-369-186-15	Sequence 15, Appli
c 8	21	100.0	396	13	US-10-361-811-15	Sequence 15, Appli
c 9	21	100.0	396	16	US-10-212-677-15	Sequence 15, Appli
c 10	21	100.0	461	11	US-09-918-995-32172	Sequence 32172, A
c 11	21	100.0	462	11	US-09-918-995-32172	Sequence 2524, Ap
c 12	21	100.0	465	11	US-09-918-995-32177	Sequence 32177, A
c 13	21	100.0	492	11	US-09-918-995-31156	Sequence 31156, A
c 14	21	100.0	532	10	US-09-831-381-910	Sequence 910, Appli
c 15	21	100.0	539	11	US-09-918-995-31688	Sequence 31688, A

RESULT 2
 US-09-967-726A-5

```

; Sequence 5, Application US/09947726A
; Publication No. US20030138130A1.
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Zellweger, Tobias
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2 Oligonucleotides
; FILE REFERENCE: UBC_P-022
; CURRENT APPLICATION NUMBER: US/09/967,726A
; CURRENT FILING DATE: 2001-09-28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
; US-09-967-726A-5

Query Match      100.0%  Score 21;  DB 13;  Length 21;
Best Local Similarity 100.0%  Pred. No. 0.57;
Matches 21;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 ATTTGCTGAGACCGCTCTGGTC 21
Db      1 ATTTGCTGAGACCGCTCTGGTC 21

; RESULT 3
; US-10-080-794-5
; Sequence 5, Application US/10080794
; Publication No. US20030166591A1.
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
; TITLE OF INVENTION: HAVING 2'-O-(2-METHOXY) ETHYL MODIFICATIONS
; FILE REFERENCE: UBC_P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/513,325
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/944,326
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
; US-10-080-794-5

Query Match      100.0%  Score 21;  DB 13;  Length 21;
Best Local Similarity 100.0%  Pred. No. 0.57;
Matches 21;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

; RESULT 4
; US-10-044-579-14/C
; Sequence 4, Application US/09944579
; Publication No. US20030138130A1.
; GENERAL INFORMATION:
; APPLICANT: Kirschling, Deborah J.
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B.
; TITLE OF INVENTION: Genes and Genetic Elements Associated with Sensitivity to Cisplatin
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; PRIORITY APPLICATION NUMBER: US/10/404,579
; PRIORITY APPLICATION DATA:
; PRIORITY APPLICATION NUMBER: US/08/485,657A
; PRIORITY APPLICATION DATA:
; PRIORITY APPLICATION NUMBER: US/09/9591A1
; PRIORITY APPLICATION DATA:
; PRIORITY APPLICATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
; US-10-044-579-14

Query Match      100.0%  Score 21;  DB 12;  Length 195;
Best Local Similarity 100.0%  Pred. No. 0.57;
Matches 21;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 ATTTCTGAGACCTCTGGTC 21
Db      153 ATTTCTGAGACCTCTGGTC 133

; RESULT 5
; US-09-805-294-15/C
; Sequence 15, Application US/09825294
; Publication No. US2002004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Aigate, Paul A.
; APPLICANT: Fing, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121-4845
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 15
; LENGTH: 396
; TYPE: DNA
; 
```

ORGANISM: Homo sapien
 FEATURE: misc_feature
 LOCATION: (1) . (96)
 OTHER INFORMATION: n = A,T,C or G

US-09-835-294-15

Query Match 100.0%; Score 21; DB 9; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTTCTGAGACCTCTGTC 21
 Db 145 ATTTCTGAGACCTCTGTC 125

RESULT 6
 US-09-970-966-15/C
 Sequence 15, Application US/0970966
 Patent No. US200173638A1
 GENERAL INFORMATION:
 APPLICANT: Stolk, John A.
 APPLICANT: Molesh, David Alan
 APPLICANT: Fling, Steven P.
 APPLICANT: Xu, Jiaochun
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 AND DIAGNOSIS OF OVARIAN CANCER
 FILE REFERENCE: 210121.484C6
 CURRENT FILING DATE: 2001-10-02
 NUMBER OF SEQ ID NOS: 215
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 15
 LENGTH: 396
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE: misc_feature
 LOCATION: 333
 OTHER INFORMATION: n = A,T,C or G

US-09-970-966-15

Query Match 100.0%; Score 21; DB 10; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTTCTGAGACCTCTGTC 21
 Db 145 ATTTCTGAGACCTCTGTC 125

RESULT 7
 US-10-369-186-15/C
 Sequence 15, Application US/10369186
 Publication No. US20030232056A1
 GENERAL INFORMATION:
 APPLICANT: Fanger, Gary R.
 APPLICANT: Fling, Steven P.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 AND DIAGNOSIS OF OVARIAN CANCER
 FILE REFERENCE: 210121.484C7
 CURRENT FILING DATE: 2003-02-14
 NUMBER OF SEQ ID NOS: 293
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 15
 LENGTH: 396
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE: misc_feature
 LOCATION: 333
 OTHER INFORMATION: n = A,T,C or G

US-10-369-186-15

Query Match 100.0%; Score 21; DB 12; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTTCTGAGACCTCTGTC 21
 Db 145 ATTTCTGAGACCTCTGTC 125

RESULT 8
 US-10-361-811-15/C
 Sequence 15, Application US/10361811
 Publication No. US20030206918A1
 GENERAL INFORMATION:
 APPLICANT: Fanger, Gary R.
 APPLICANT: Fling, Steven P.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 AND DIAGNOSIS OF OVARIAN CANCER
 FILE REFERENCE: 210121.484C8
 CURRENT APPLICATION NUMBER: US/10/361,811
 CURRENT FILING DATE: 2003-02-05
 NUMBER OF SEQ ID NOS: 293
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 15
 LENGTH: 396
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE: misc_feature
 LOCATION: 333
 OTHER INFORMATION: n = A,T,C or G

US-10-361-811-15

Query Match 100.0%; Score 21; DB 13; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTTCTGAGACCTCTGTC 21
 Db 145 ATTTCTGAGACCTCTGTC 125

RESULT 9
 US-10-212-677-15/C
 Sequence 15, Application US/10212677
 Publication No. US2003129192A1
 GENERAL INFORMATION:
 APPLICANT: Chenault, Ruth A.
 APPLICANT: Xu, Jiangchun
 APPLICANT: Harlicker, Susan L.
 APPLICANT: McNeill, Patricia D.
 APPLICANT: Fanger, Gary R.
 APPLICANT: Harlicker, Susan L.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 AND DIAGNOSIS OF OVARIAN CANCER
 FILE REFERENCE: 210121.484C7
 CURRENT APPLICATION NUMBER: US/10/212,677
 CURRENT FILING DATE: 2002-08-02
 NUMBER OF SEQ ID NOS: 288
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 15
 LENGTH: 396
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE: misc_feature
 LOCATION: 333
 OTHER INFORMATION: n = A,T,C or G

US-10-212-677-15

Query Match 100.0%; Score 21; DB 16; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.58;

Patent No. US20020132090A1
 GENERAL INFORMATION:
 APPLICANT: Robison, Keith E.
 TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs
 FILE REFERENCE: 5800-119
 CURRENT APPLICATION NUMBER: US09/033,381
 CURRENT FILING DATE: 2001-04-11
 PRIOR APPLICATION NUMBER: 09/516,448
 PRIOR FILING DATE: 2000-02-29
 NUMBER OF SEQ ID NOS: 2050
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 910
 LENGTH: 532
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)...(532)
 OTHER INFORMATION: n = A,T,C or G
 US-09-833-381-910

Query Match 100.0%; Score 21; DB 10; Length 532;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATTTGTCAGAGCCGTGTC 21
 Db 159 ATTTGTCAGAGCCGTGTC 139

RESULT 15
 US-09-918-995-21688/C
 Sequence 31688, Application US/0918995
 Publication No. US20030073623A1
 GENERAL INFORMATION:
 APPLICANT: Hyseq, Inc.
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 FILE REFERENCE: 20411-756
 CURRENT APPLICATION NUMBER: US/09/918,995
 CURRENT FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: US/09/235,076
 PRIOR FILING DATE: 1999-01-20
 NUMBER OF SEQ ID NOS: 38054
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 31688
 LENGTH: 539
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)...(539)
 OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-31688

Query Match 100.0%; Score 21; DB 11; Length 539;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATTTGTCAGAGCCGTGTC 21
 Db 207 ATTTGTCAGAGCCGTGTC 187

Search completed: January 21, 2004, 15:35:43
 Job time : 224 secs

This Page Blank (uspto)

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using SW model	Run on:	Result No.	Query Match Length DB ID	Description
Title: US-09-913-325-12		c 1	21 100.0	975 6 AX014321 Sequence
Perfect score: 21	Sequence: 1 gctggccggatggggccat 21	c 2	21 100.0	1416 6 AR210755 Sequence
Scoring table: IDENTITY_NUC		c 3	21 100.0	1416 9 HUMSGLY
Gapop 10_0 , Gapext 1.0		c 4	21 100.0	1512 6 AX302541 Sequence
Searched: 2888711 seqs, 20454813386 residues	Total number of hits satisfying chosen parameters: 5777422	c 5	21 100.0	1512 9 HUMAPQJ
Post-processing: Minimum Match 0%	Maximum DB seq length: 0	c 6	21 100.0	1546 9 AK093399 Sequence
Minimum DB seq length: 20000000000	Listing first 45 summaries	c 7	21 100.0	1648 6 AR208704 Sequence
Database : GenEmbl:*		c 8	21 100.0	1648 9 HUMTRPM2A
1: gb_ba:*		c 9	21 100.0	1658 9 BC019588
2: gb_ntg:*		c 10	21 100.0	1676 9 HSCSP240
3: gb_in:*		c 11	21 100.0	1678 6 AX202086 Sequence
4: gb_om:*		c 12	21 100.0	1684 9 BC010514 Homo sapi
5: gb_ov:*		c 13	21 100.0	1706 6 AX330207 Sequence
6: gb_dat:*		c 14	21 100.0	3196 6 AX33122 Sequence
7: gb_ph:*		c 15	21 100.0	3196 9 HUMTRPM2A4
8: gb_dl:*		c 16	21 100.0	8133 6 AR208711 Sequence
9: gb_bp:*		c 17	21 100.0	8133 9 HUMSP1040A
10: gb_ro:*		c 18	21 100.0	134514 2 AC025192 Homo sapi
11: gb_sts:*		c 19	21 100.0	234431 9 AF311103 Homo sapi
12: gb_sy:*		c 20	21 100.0	334051 2 AC123374 Rattus no
13: gb_un:*		c 21	18.4	87.6 57722 2 HSCB33310 Homo sapi
14: gb_vl:*		c 22	18.4	87.6 76295 2 AC023542 Homo sapi
15: em_da:*		c 23	18.4	87.6 10608 9 HS506
16: em_fun:*		c 24	18.4	87.6 147895 12 SYNSVAPYRO
17: em_hum:*		c 25	17.8	84.8 2132 9 HSA011802
18: em_in:*		c 26	17.8	84.8 67396 9 AC008848
19: em_mu:*		c 27	17.8	84.8 113384 2 AC012411 Felis cat
20: em_om:*		c 28	17.8	84.8 113384 2 AC012617 Homo sapi
21: em_or:*		c 29	17.8	84.8 126590 9 AC012617
22: em_ov:*		c 30	17.8	84.8 13991 10 AC09047
23: em_dat:*		c 31	17.8	84.8 152223 2 AC119192
24: em_ph:*		c 32	17.8	84.8 157758 9 AC098824
25: em_bp:*		c 33	17.8	84.8 169638 9 AC014433
26: em_ro:*		c 34	17.8	84.8 178862 9 AC011847
27: em_vl:*		c 35	17.8	84.8 185854 2 AC027736
28: em_in:*		c 36	17.8	84.8 190337 2 AC103477
29: em_vl:*		c 37	17.8	84.8 220558 2 AC129036
30: em_ntg_hum:*		c 38	17.8	84.8 266943 2 AC095241
31: em_ntg_irv:*		c 39	17.8	84.8 300425 1 AP005022
32: em_ntg_other:*		c 40	17.4	82.9 3615 6 AX505167 Sequence
33: em_ntg_mus:*		c 41	17.4	82.9 3732 6 AX505243 Sequence
34: em_ntg_p11:*		c 42	17.4	82.9 14642 10 AF530161
35: em_ntg_rod:*		c 43	17.4	82.9 114669 9 AC105186
36: em_ntg_man:*		c 44	17.4	82.9 160513 2 AC144696
37: em_ntg_vrt:*		c 45	17.4	82.9 175934 2 AC123868 Mus muscu

ALIGNMENTS

RESULT ¹	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
AX014321/c	AX014321	Sequence 29 from Patent WO9543353.	AX014321	AX014321.1	GI:1040675	Homo sapiens (human)	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 Schmitt, A., Specht, T., Dahl, E., Hirzmann, B., Rosenthal, A. and Pillarky, C.			

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 9954353-A 29 28-OCT-1999;
 SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
 BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUNG
 (DE); PILARSKY CHRISTIAN (DE)

FEATURES source

LOCUS 1. .975
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /map="8"
 /sex="male"
 /cell_type="astrocytoma (gr.III)"
 /tissue_type="brain tumor"
 /dev_stage="63 yr. old adult"

BASE COUNT 221 a 320 c 248 g 186 t

ORIGIN Query Match 100.0%; Score 21; DB 6; Length 975;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGGGAGTTGGGGCT 21
 Db 903 GCTGGGGAGTTGGGGCT 883

RESULT 2 AR270755/c AR270755 1416 bp DNA linear PAT 10-APR-2003
 DEFINITION Sequence 1318 from patent US 6500938.
 ACCESSION AR270755
 VERSION AR270755.1
 KEYWORDS UNKNOWN
 ORGANISM UNKNOWN
 SOURCE UNKNOWN.
 REFERENCE 1 (bases 1 to 1416)
 AUTHORS Au-Young J. and Seilhamer,J.J.
 TITLE Composition for the detection of signaling pathway gene expression
 JOURNAL Patent: US 6500938.A 31-DEC-2002;
 FEATURES Location/Qualifiers
 SOURCE 1. .1416
 /organism="unknown" 267 t

BASE COUNT 344 a 440 c 365 g

ORIGIN 267 t

Query Match 100.0%; Score 21; DB 6; Length 1416;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGGGAGTTGGGGCT 21
 Db 1309 GCTGGGGAGTTGGGGCT 1289

RESULT 3 HUMSGLY HUMSGLY 1416 bp mRNA linear PRI 09-JAN-1995
 DEFINITION Human sulfated glycoprotein-2 mRNA, 3' end.
 ACCESSION M74816
 VERSION 1 (bases 1 to 1416)
 KEYWORDS secreted protein; sulfated glycoprotein-2.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Mammalia; Etheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 Danik,M., Chabot,J.G., Mercier,C., Benabid,A.L., Chauvin,C.,
 Quirion,R. and Sub,M.
 Human gliomas and epileptic foci express high levels of a mRNA
 related to rat testicular sulfated glycoprotein 2, a purported
 marker of cell death
 Proc. Natl. Acad. Sci. U.S.A. 88 (19), 8577-8581 (1991)

REFERENCE 1924317
 JOURNAL MEDLINE
 MEDLINE 3200896
 PUBLISHED 1924317
 COMMENT Original source text: Homo sapiens male 63 yr. old adult brain
 tumor cDNA to mRNA.
 FEATURES Location/Qualifiers

RESULT 4 AX302541/c AX302541
 LOCUS AX302541
 DEFINITION Sequence 59 from Patent WO0175177.
 ACCESSION AX302541
 VERSION AX302541.1 GI:17383080
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Morin, P. J., Sherman-Baust, C. A., Pizer, E. S. and Hough, C. D.
 TITLE Patent: WO 0175177-A 59 11-OCT-2001;
 JOURNAL THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
 FEATURES Location/Qualifiers
 SOURCE 1. .1512
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 BASE COUNT 378 a 461 c 387 g 286 t

Query Match 100.0%; Score 21; DB 6; Length 1512;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGGGAGTTGGGGCT 21
 Db 1405 GCTGGGGAGTTGGGGCT 1385

RESULT 5 HUMAPOJ/c HUMAPOJ
 LOCUS 1512 bp mRNA linear

DEFINITION Human apolipoprotein J mRNA, complete cds.

ACCESSION J02908

VERSION .1

KEYWORDS apolipoprotein J; high density lipoprotein.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE AUTHORS Nishi,T., Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Sugiyama,T., Irie,R., Otsuki,T., Saito,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kaneshori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawai-K., Nagai,K., Sugano,S., Nacahara,K., Matsuo,Y., Nagai,K. and Isogai,T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REMARKS 2 (bases 1 to 1546)

REFERENCE AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

COMMENT (E-mail:genomics@nri.co.jp, Tel: 81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES Location/Qualifiers

source 1..1546 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="RAXON:9606"

source 1..1512 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="Unassigned"

source 1..1512 /gene="APOJ"
/product="apolipoprotein J mRNA"
/db_xref="GDB:13052"
/gene="APOJ"
/note="apolipoprotein J precursor"
/codon_start=1
/protein_id="AA51765.1"
/db_xref="ICI:178855"
/db_xref=GDB:13052
/translation="MSNOQSKYVNEKIQNAVNGYKQIKLIEKNEERKTLISNLNEA
KKKKEDAINTRESTPKLKEPLPGVNETMAMLNECKPKLQKTCMKEYARVRSRSGLQ
VGRQEEFLINQSSPFYFWNGDRIFLLENDRQTHMLDVMQHPSRASSIDELQD
RFFTEPQDITYHSPFQCHPTEPQFREGDDDTTCREIRNSTGCLRMKDQDCREIQL
HEAQGMDTIEHSFPAFQCHPTEPQFREGDDDTTCREIRNSTGCLRMKDQDCREIQL
SVIDCSPNPSAQLRNLQVLLKNSQWQMNNTSSLEQDNEQNS
WVSRNLNLTOQDQYLRYTVTVASTISDSDPTEVVVLFDSDFITVVEVSR
KKNPKMKTVAEKAQLEYRKKREE"

mat_peptide 18..599 /gene="APOJ"
/product="apolipoprotein J alpha-subunit"
/db_xref="GDB:13052"
/gene="APOJ"
/product="apolipoprotein J beta-subunit"

mat_peptide 600..1265 /gene="APOJ"
/product="apolipoprotein J beta-subunit"

BASE COUNT 378 a /product="apolipoprotein J beta-subunit"
ORIGIN 387 g 286 t

Query Match 100.0% Score 21; DB 9; Length 1512; PRI 15-JUL-2002
Best Local Similarity 100.0%; Pred. No. 45; Mismatches 0; Indels 0; Gaps 0;

BASE COUNT 1 GCTGGCGGAGTGGGGGCT 21
ORIGIN 1385

Query Match 100.0% Score 21; DB 9; Length 1512; PRI 15-JUL-2002
Best Local Similarity 100.0%; Pred. No. 45; Mismatches 0; Indels 0; Gaps 0;

BASE COUNT 1 GCTGGCGGAGTGGGGGCT 21
ORIGIN 1541 GCTGGCGGAGTGGGGGCT 1521

49. .11398
 /codon_start=1
 /product="Clusterin (complement lysis inhibitor, SP-40,40,
 sulfated glycoprotein 2, testosterone-repressed prostate
 message 2, apo-1 protein in J)."!
 /protein_id="AAH19888.1"
 /db_xref="GI:18043615"
 /db_xref=LocusID:1191"
 /translation="MMMKULLFVGLLTLWESGOVLDOTVSNEQMSQGSKYVNRK
 SIQNAVNGVQKQKLEKERNERKRTLNSLAEKKKKEDALNNETRESETKLKELPLGVC
 NETMMALWECKPKCLQKQTLFVYKVRGSGLYVQDLEELNQSPFVYFVWNGDRID
 SLLENDRQOQHMLDYMQDFRSASSIIDLFDQDFTRPDDTHYLFLSPHRRPHF
 FEPKSRSIVSPLMPSPYEPFLNPHAMQPFLEMTHAACAMDTHFSPAFQHPTEEFR
 EGRDIDKTVCEIRKRDGCLKQDCKDCNNPSQAKLRFELDESLOQVA
 ERLTAKYKNEILKSTKOMKNTSLLQEQLNEQVNRSLANLQEQDQYLRLTVVASH
 TSDSDVPSGTCVTVVVKLFPSDPIVTVPEVSRNPKEMETAKALQEQYRKXHREE"
 BASE COUNT 423 a 486 c 439 g 310 t
 ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1658;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 21; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTGGGGCCT 21
 Db 1535 GCTGGCGGAGTGGGGCCT 1515

RESULT 10
 HS2SP40/c HSCP40 1676 bp mRNA linear PRI 22-MAR-1995
 LOCUS Human SP-40,40 mRNA for complement-associated protein SP-40,40
 DEFINITION alpha-1 and beta-1 chain.
 ACCESSION X14723
 VERSION X14723.1 GI:30250
 KEYWORDS complement-associated protein; serum protein; SP-40,40 gene.
 ORGANISM Homo sapiens (human)
 SOURCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1. (bases 1 to 1676)
 AUTHORS Kirschbaum, L., Sharpe, J.A., Murphy, B., d'Apice, A.J., Classon, B.,
 Hudson, P. and Walker, I.D.
 TITLE Molecular cloning and characterization of the novel, human
 complement-associated protein, SP-40,40: a link between the
 complement and reproductive systems
 JOURNAL EMBO J. 8 (3), 711-718 (1989)
 MEDLINE 8921601
 PUBLMED 2721439
 REFERENCE 2 (bases 1 to 1676)
 AUTHORS Kirschbaum, L.
 JOURNAL Direct Submission
 Submitted (17-MAR-1999) Kirschbaum L., The University of Melbourne,
 The Precinct Clinical Centre, School of Veterinary Science, Parkville
 Victoria 3052 Australia
 COMMENT The sequence overlaps with that reported by Murphy et. al. in J.
 J. Clin. Invest. 8:1858-1864 (1988).
 FEATURES Location/Qualifiers
 1. .1676
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="LK (107)"
 /tissue_type="liver"
 /clone_Lib="Lambda g51"
 48. .11397
 /note="SP-40,40 prepropeptide (AA -22 to 427)"
 /codon_start=1
 /protein_id="CAA32847.1"
 /db_xref="GI:30251"
 /db_xref="SWISS-PROT:PI0909"
 /translation="MMMKULLFVGLLTLWESGOVLDOTVSNEQMSQGSKYVNRK
 SIQNAVNGVQKQKLEKERNERKRTLNSLAEKKKKEDALNNETRESETKLKELPLGVC
 NETMMALWECKPKCLQKQTLFVYKVRGSGLYVQDLEELNQSPFVYFVWNGDRID
 SLLENDRQOQHMLDYMQDFRSASSIIDLFDQDFTRPDDTHYLFLSPHRRPHF
 FEPKSRSIVSPLMPSPYEPFLNPHAMQPFLEMTHAACAMDTHFSPAFQHPTEEFR
 ERLTAKYKNEILKSTKOMKNTSLLQEQLNEQVNRSLANLQEQDQYLRLTVVASH
 TSDSDVPSGTCVTVVVKLFPSDPIVTVPEVSRNPKEMETAKALQEQYRKXHREE"
 BASE COUNT 423 a 486 c 439 g 310 t
 ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1676;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 21; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTGGGGCCT 21
 Db 1536 GCTGGCGGAGTGGGGCCT 1516

RESULT 11
 AX2202086/c AX2202086 1678 bp DNA linear PAT 30-AUG-2001
 LOCUS Sequence 16 From Patent WO0153531.
 DEFINITION AX2202086
 ACCESSION AX2202086.1 GI:15391872
 VERSION
 KEYWORDS SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1. (bases 1 to 1678)
 AUTHORS Phippard, D.; Vassanthakamur, G.; Dotson, S. and Ma, X.J.
 TITLE Osteoarthritis tissue derived nucleic acids, polypeptides, vectors,
 and cells
 JOURNAL Patent: WO 0153531-A 16-26-JUL-2001;
 Pharmacia Corporation (US)
 FEATURES Location/Qualifiers
 1. .1678
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /db_xref="taxon:9606"
 BASE COUNT 424 a 491 c 450 g 313 t
 ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 1678;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 21; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTGGGGCCT 21
 Db 1558 GCTGGCGGAGTGGGGCCT 1538

RESULT 12
 BC010514/c BC010514 1664 bp mRNA linear PRI 17-APR-2003
 LOCUS Homo sapiens cluasterin (complement lysis inhibitor, SP-10,40,
 DEFINITION sulfated glycoprotein 2, testosterone-repressed protease message 2,
 apolipoprotein J), mRNA (cDNA clone MGC:18080 IMAGE:4150452),
 complete cds.
 ACCESSION BC010514
 VERSION BC010514.1
 KEYWORDS SOURCE Homo sapiens (human)

48. .11397
 /note="SP-40,40 prepropeptide (AA -22 to 427)"
 /codon_start=1
 /protein_id="CAA32847.1"
 /db_xref="GI:30251"
 /db_xref="SWISS-PROT:PI0909"
 /translation="MMMKULLFVGLLTLWESGOVLDOTVSNEQMSQGSKYVNRK
 SIQNAVNGVQKQKLEKERNERKRTLNSLAEKKKKEDALNNETRESETKLKELPLGVC
 NETMMALWECKPKCLQKQTLFVYKVRGSGLYVQDLEELNQSPFVYFVWNGDRID
 SLLENDRQOQHMLDYMQDFRSASSIIDLFDQDFTRPDDTHYLFLSPHRRPHF
 FEPKSRSIVSPLMPSPYEPFLNPHAMQPFLEMTHAACAMDTHFSPAFQHPTEEFR
 ERLTAKYKNEILKSTKOMKNTSLLQEQLNEQVNRSLANLQEQDQYLRLTVVASH
 TSDSDVPSGTCVTVVVKLFPSDPIVTVPEVSRNPKEMETAKALQEQYRKXHREE"
 BASE COUNT 423 a 486 c 439 g 310 t
 ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1676;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 21; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTGGGGCCT 21
 Db 1536 GCTGGCGGAGTGGGGCCT 1516

ORGANISM	Homo sapiens	COMMENT	
MATERIAL	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	REFERENCE	1 (bases 1 to 1684)
AUTHORS	Strausberg,R.L., Collings,B.A., Grouse,I.H., Derge,J.G., Altenschul,S.F., Zeeberg,B., Buerow,K.H., Schaefer,C.P., Bhat,N.K., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleron,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiaki,S., Carninci,P., Prange,C., Raha,S.S., Loqueland,N.A., Peters,G.J., Abramson,R.D., Mullally,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulik,R.S.W., Villalon,D.K., Muzny,D.N., Sodergren,E.J., Lu,X., Gibbs,R.A., Bahay,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krywinski,M.I., Skalska,U., Smalius,D.E., Schnerch,A., Schein,J.E., Jones,S.J., and Marra,M.A.	REFERENCE	1 (bases 1 to 1684)
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	JOURNAL	PROC. NATL. ACAD. SCI. U.S.A. 99 (26), 16899-16903 (2002)
FEATURES	2 (bases 1 to 1684)	COMMENT	
AUTHORS	Strausberg,R.	COMMENT	
JOURNAL	Direct Submission	COMMENT	
FEATURES	Submitted (10-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC) Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	COMMENT	
AUTHORS	NIH-MGC Project URL: http://mgc.ncbi.nih.gov	COMMENT	
JOURNAL	Contact: MGC help desk	COMMENT	
FEATURES	Email: cgbps-f@mail.nih.gov	COMMENT	
AUTHORS	Tissue Procurement: David N. Louis, M.D.	COMMENT	
JOURNAL	CDNA Library Preparation: Life Technologies, Inc.	COMMENT	
FEATURES	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)	COMMENT	
AUTHORS	DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center	COMMENT	
JOURNAL	Center code: BCM-HGSC	COMMENT	
FEATURES	Web site: http://www.hgsc.bcm.edu/cDNA/	COMMENT	
AUTHORS	Contact: amg@bcm.tmc.edu	COMMENT	
JOURNAL	Series: ITRAK Plate: 19 Row: o Column: 12.	COMMENT	
FEATURES	Location/Qualifiers	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/note="synonyms: APOJ, CLI, SP-40, SGP-2, TRPM-2, TRPM2"	COMMENT	
FEATURES	/db_xref="LocusID:1191"	COMMENT	
AUTHORS	/db_xref="MIM:185430"	COMMENT	
JOURNAL	/codon_Start=1	COMMENT	
FEATURES	/product="clusterin (complement lysis inhibitor, SP-40, 40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)"	COMMENT	
AUTHORS	69-1418	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
JOURNAL	/lab_host="CHI08"	COMMENT	
FEATURES	/note="Vector: pCMV-SPORT6"	COMMENT	
AUTHORS	TRPM2	COMMENT	
JOURNAL	/db_xref="LocusID:1191"	COMMENT	
FEATURES	/db_xref="MIM:185430"	COMMENT	
AUTHORS	69	COMMENT	
JOURNAL	/note="Vector: pCMV-SPORT6"	COMMENT	
FEATURES	/gen="C11U"	COMMENT	
AUTHORS	1-1684	COMMENT	
J			

gene sets

JOURNAL Patent : WO 0194629-A 7631_13-DEC-2001;
Avalon Pharmaceuticals (US)

FEATURES Location/Qualifiers

source 1. .3196

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 833 a -762 c 789 g 812 t

ORIGIN

RESULT 15

HUMTRPM2A4/c

LCUS HUMTRPM2A4 3196 bp DNA linear PRI 23-AUG-1996

DEFINITION Human TRPM-2 protein gene, exons 7,8,9 and complete cds.

ACCESSION M63379

VERSION M63379.1

KEYWORDS TRPM-2, Protein.

SEGMENT 4 of 4

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates;

REFERENCE Wong, P., Pineault, J., Lakins, J., Taillefer, D., Leger, J., Wang, C. and Tenniswood, M.

AUTHORS Wong, P., Pineault, J., Lakins, J., Taillefer, D., Leger, J., Wang, C.

TITLE Genomic organization and expression of the rat TRPM-2 (clusterin)

JOURNAL J. Biol. Chem. 268 (7), 5021-5031 (1993)

MEDLINE 93186813

PUBLISHED 2 (bases 1 to 3196)

AUTHORS Wong, P., Taillefer, D., Lakins, J., Pineault, J., Chader, G. and Tenniswood, M.

TITLE Molecular characterization of human TRPM-2/clusterin, a gene associated with sperm maturation, apoptosis and neurodegeneration

Eur. J. Biochem. 222. (3), 917-925 (1994)

MEDLINE 94237156

PUBLISHED 818144

COMMENT Original source text: Homo sapiens DNA.

FEATURES source

Location/Qualifiers

1. .3196

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="exon:9606"

join(M63376.1:1422..7610,M63377.1:1..940,M63378.1:1..1634,
M63376.1:7021..7169,M63377.1:1..559..5634,
M63378.1:1247..1351..995..1224..2362..2537..2745..2998)

gene

mRNA

CDS

/gene="TRPM-2"
/join(M63376.1:5538..5634..M63376.1:7021..7169,
M63377.1:155..325..M63378.1:308..719..M63378.1:1247..1351,
995..1224..2362..2537..2745..2754)

/gene="TRPM-2"
/codon_start=1
/protein_id="AAB06507_1"
/db_xref="GI:292843"
/translation="MMKTLKLLFVGLLGLLWESQVLDQTVSDNELOQEMSNQGSKVNK
EIONAVNGVKQDQKIKLTKLNPERKTKLNSLNEAKKKEDAEANESETKELPGVC
NEITMNAWECKBPLKQCKMFKYARVRSQSSLVQOLEELINQSSPFYPMANGRID
SLLENDROTHIMLDVMDHFSASSIDELFDQRFTRPDTYILPFSPLPHRF
FFPKSRIVSLMFSPTPEPLNFMHQPFMTHQACQAMJHFSAPQGPPTFIR

This Page Blank (uspto)

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 10:04:17 ; Search time 148 Seconds
 (without alignments)
 383.028 Million cell updates/sec

Title: US-09-913-325-12
 Perfect score: 21
 Sequence: 1 gctggggggatggggcct 21

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseg_19Jun03,*
 1: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1980.DAT:*

2: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1981.DAT:*

3: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1982.DAT:*

4: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1983.DAT:*

5: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1984.DAT:*

6: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1985.DAT:*

7: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1986.DAT:*

8: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1987.DAT:*

9: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1988.DAT:*

10: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1989.DAT:*

11: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1990.DAT:*

12: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1991.DAT:*

13: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1992.DAT:*

14: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1993.DAT:*

15: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1994.DAT:*

16: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1995.DAT:*

17: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1996.DAT:*

18: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1997.DAT:*

19: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1998.DAT:*

20: /SIDS1/gcdata/geneseg/genesegn-emb1/NA1999.DAT:*

21: /SIDS1/gcdata/geneseg/genesegn-emb1/NA2000.DAT:*

22: /SIDS1/gcdata/geneseg/genesegn-emb1/NA2001A.DAT:*

23: /SIDS1/gcdata/geneseg/genesegn-emb1/NA2001B.DAT:*

24: /SIDS1/gcdata/geneseg/genesegn-emb1/NA2002.DAT:*

25: /SIDS1/gcdata/geneseg/genesegn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	21	100.0	21	21	A2294214	Human testosterone
C 2	21	100.0	975	20	AAC21353	Human normal uterus
C 3	21	100.0	1416	25	AC56720	Human signalling P
C 4	21	100.0	1512	22	AB83111	Apolipoprotein J
C 5	21	100.0	1648	24	ABN1656	Human luteinizing
C 6	21	100.0	1678	22	AH23086	Osteoarthritis tis
C 7	21	100.0	2876	21	AAC90467	Human uncoupling P
C 8	21	100.0	3196	24	ABE62379	Colon adenocarcino

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Alignments	RESULTS	1	AAA94234	standard; DNA; 21 BP.
	ID	AAA94234		
	XX			
	AC			
	AAA94234;			
	XX			
	DT			
	12-JAN-2001			
	(first entry)			
	XX			
	DE			
	Human testosterone-repressed prostate message-2 antisense oligo #10.			
	XX			
	DR			
	Human: testosterone-repressed prostate message-2; TRPM-2; clusterin; KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.			
	XX			
	KW			
	Human sapiens.			
	XX			
	OS			
	XX			
	PW			
	W0200049337-A2.			
	XX			
	PD			
	31-AUG-2000.			
	XX			
	PP			
	25-FEB-2000; 2000W0-US04875.			
	XX			
	PR			
	26-FEB-1999;			
	99US-0121726.			
	XX			
	(UYBR-)			
	UNIV BRITISH COLUMBIA.			
	PA			
	XX			
	PI			
	Gleave M, Renie PS, Miyake H, Nelson C,			
	XX			
	DR			
	WPI; 2000-533132/48.			
	XX			
	PT			
	Treating prostatic tumors and renal cancers by antisense inhibition of the testosterone-repressed prostate messenger-2 gene -			
	PT			

XX	SQ	Sequence 1416 BP; 344 A; 440 C; 365 G; 267 T; 0 other;
XX	Query Match	100 %; Score 21; DB 25; Length 1416;
XX	Best Local Similarity	100 %; Pred. No. 13;
XX	Matches 21;	Conservative 0; Mismatches 0; Indels 0; Caps 0;
Qy	1	GCTGGGGAGTGGGGCCT 21
Db	1309	GCTGGGGAGTGGGGCCT 1289
RESULT 4		
XX	ID	ABA83111/C
XX	ID	ABA83111 standard; DNA; 1512 BP.
XX	AC	ABA83111;
XX	AC	ABA83111;
DT	08-FEB-2002	(first entry)
XX	DE	Apolipoprotein J ovarian tumour marker gene, SEQ ID NO:59.
XX	DE	human; overexpression; upregulation; epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;
XX	KW	serous cystadenocarcinoma; mucinous cystadenocarcinoma;
XX	KW	borderline serous tumour; mucinous cystadenoma;
XX	KW	borderline mucinous tumour; endometrioid carcinoma;
XX	KW	adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE; immune response Pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic; gene therapy; vaccine; ds.
XX	KW	Homo sapiens.
OS	XX	WO200175177-A2.
PN	XX	PD 11-OCT-2001.
PN	XX	PP 03-APR-2001; 2001WO-US10947.
PN	XX	PR 03-APR-2000; 2000US-194336P.
PA	XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.
PA	XX	Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;
PR	XX	WPI: 2001-626450/72.
DR	XX	P-PSDB; ABB50285.
DR	XX	Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker gene.
PR	XX	Claim 23; Page 103; 140pp; English.
CC	XX	The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180, ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179, ABA83181 and ABA83183). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for assessing the relative severity of ovarian cancer, in tests for monitoring a patient in remission from ovarian cancer and in tests for monitoring disease status in a patient being treated for ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour (i.e., an epithelial ovarian tumour selected from serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma, mucinous cystadenoma, borderline mucinous tumour, mucinous cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner.

The ovarian tumour marker genes of the invention were identified using SAGE (serial analysis of gene expression) and were found to be overexpressed in a broad variety of ovarian epithelial tumour cells relative to normal ovarian epithelial cells. The marker genes are implicated in immune response pathways, in the regulation of cell proliferation and in protein folding, and many of these are membrane-localised or secreted. In addition to their use as diagnostic and prognostic markers, the ovarian tumour marker genes or their encoded proteins may be used as therapeutic targets for the treatment and prevention of ovarian cancer. Sequences ABAB3081-ABAB3122, ABAB3180, ABAB3182 and ABAB3184 represent the ovarian tumour marker genes of the invention.

Best Local Similarity	100.0%	Pred.	No. 13;	XX	DT	12-MAR-2001	(first entry)
Matches	21;	Conservative	0;	Mismatches	0;	Indels	0;
Qy	1 GCTGGCGGAGTTGGGGCT	21		0;	Gaps	0;	
Db	1541 GCTGGCGGAGTTGGGGCT	1521					
RESULT 6							
AAH23086/C							
ID	AAH23086	standard;	DNA;	1678	BP.		
XX							
AC	AAH23086;						
XX							
DT	17-SEP-2001	(first entry)					
XX							
DB	Osteoarthritis tissue-derived nucleic acid sequence #16.						
XX							
KW	Osteoarthritis; infectious disorder; Crohn's disease; sepsis; human;						
KW	wound healing; osteopathic; antiarthritic; anti-inflammatory;						
KW	vulnerary; antibacterial; antiallergic; ds.						
OS	Homo sapiens.						
XX							
PN	WO200153531-A2.						
XX							
PA	26-JUL-2001.						
XX							
PI	Ruben SM, Ni J, Komatsu S, G, Rosen CA, Soppet DR;						
XX							
PR	18-JAN-2001; 2001WO-US00016.						
XX							
PA	(PHJA) PHARMACIA CORP.						
XX							
PI	Phippard D, Vasanthakamur G, Dotson S, Ma X;						
XX							
DR	2001-451914/48.						
XX							
PS	Substantially purified protein, polypeptide or their fragments, used to						
PT	identify a biologically active compound or composition and treat						
PT	mammalian osteoarthritis -						
XX							
PS	Claim 1; Page 102-103; 144DP; English.						
XX							
CC	Sequences AAH23071-23152 represent nucleic acid sequences derived from						
CC	osteoarthritis tissues. The sequences are useful as probes and for the						
CC	diagnosis or prognosis of mammalian osteoarthritis. The polynucleotides						
CC	and polypeptides of the invention are useful for generating diagnostic						
CC	reagents, as targets for small molecule drug development, generation of						
CC	therapeutics, and cloning genes. Specific antibodies are used to generate						
CC	enzyme linked immunosorbent assays for detection of osteoarthritis. The						
CC	invented molecules can be used to treat osteoarthritis or to analyse the						
CC	disease-modifying activity of osteoarthritis drugs. Other disorders						
CC	treatable using the nucleic acid sequences include atopic, inflammatory						
CC	and infectious disorders e.g. Crohn's disease and sepsis, and wound						
CC	healing.						
SQ	Sequence 1678 BP; 424 A; 491 C; 450 G; 313 T; 0 other;						
XX							
Query Match	100.0%	Score	21;	DB	22;	Length	1678;
Best Local Similarity	100.0%	Pred.	No. 13;	XX			
Matches	21;	Conservative	0;	Mismatches	0;	Indels	0;
Qy	1 GCTGGCGGAGTTGGGGCT	21		0;	Gaps	0;	
Db	1558 GCTGGCGGAGTTGGGGCT	1538					
RESULT 7							
AAC90467/C							
ID	AAC90467	standard;	DNA;	2876	BP.		
XX							
AC	AAC90467;						

PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237178P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244667P.
 PR 01-NOV-2000; 2000US-245084P.
 XX PA (AVAL-) AVALON PHARM.
 XX PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 DR WPI; 2002-188264/24.
 XX Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set -
 PS Claim 1; SEQ ID 7611; 44pp; English.
 XX The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL6164 to ABL7010), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity, (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Willm's tumour.
 XX Sequence 3196 BP; 833 A; 762 C; 789 G; 812 T; 0 other;
 XX Query Match Score 100.0%; Best Local Similarity 100.0%; Pred. No. 13; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX Query 1 GCTGGCGGAGTGGGGCT 21
 DB 2891 GCTGGCGGAGTGGGGCT 2871
 XX RESULT 1.0
 ID AB99663.C
 ID AB99663 standard; DNA; 8133 BP.
 XX AC AB99663;
 XX DT 16-AUG-2002 (first entry)
 XX Human Clusterin gene sequence 2.
 XX Human; antisense inhibition; antisense oligonucleotide; clusterin; KW hypercholesterolemia; cardiovascular disorder; ds; KW hyperproliferative disorder; hyperlipidemic disorder.
 XX Homo sapiens.
 XX WO200222635-A1.
 XX DR WPI; 2002-122075/16.
 XX PR 26-MAY-2000; 2000US-207484P.
 XX PA (CORI-) CORIKA CORP.
 XX PI Algate PA, Harlocker SL, Jones R;
 DE DR WPI; 2002-122075/16.
 XX PR 29-MAY-2001; 2001WO-US177556.
 XX ID AB99663 standard; DNA; 8133 BP.
 XX AC AB99663;
 XX DT 16-AUG-2002 (first entry)
 XX Human Clusterin gene sequence 2.
 XX Human; antisense inhibition; antisense oligonucleotide; clusterin; KW hypercholesterolemia; cardiovascular disorder; ds; KW hyperproliferative disorder; hyperlipidemic disorder.
 XX Homo sapiens.
 XX WO200222635-A1.
 XX DR WPI; 2002-122075/16.
 XX PR 26-MAY-2000; 2000US-207484P.
 XX PA (CORI-) CORIKA CORP.
 XX PI Algate PA, Harlocker SL, Jones R;
 DE DR WPI; 2002-122075/16.
 XX PR 29-MAY-2001; 2001WO-US177556.
 XX ID AB99663 standard; DNA; 8133 BP.
 XX AC AB99663;
 XX DT 16-AUG-2002 (first entry)
 XX Human Clusterin gene sequence 2.
 XX Human; antisense inhibition; antisense oligonucleotide; clusterin; KW hypercholesterolemia; cardiovascular disorder; ds; KW hyperproliferative disorder; hyperlipidemic disorder.
 XX Homo sapiens.
 XX WO200222635-A1.

The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (III) of a ovarian tumour polypeptide encoded by a polynucleotide sequence (S1) from the 10912 nucleotide sequence as given in ABL7023 to ABL8734, (III) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (III) can be used for detecting ovarian cancer in a patient's biological sample preferentially serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (II). (III) is useful in design and preparation of ribosome molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour cDNA library using well known techniques.

Sequence 250 BP; 61 A; 52 C; 96 G; 41 T; 0 other;

Query Match 84.8%; Score 17.8; DB 24; Length 250;
Best Local Similarity 90.5%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GCTGGCGGAGCTGGGGCT 21
Db 106 GCGGGCGGATTGGGGCT 126

RESULT 12

ID ABQ94233 standard; DNA; 3645 BP.

XX ABQ94233;

XX DT 22-OCT-2002 (first entry)

DB FLO11 gene expression regulator At11 coding sequence.

XX Fungal gene expression regulator; fungicide; gene therapy; An01; An05; An09; An10; An13; An17; An20; An28; At01-1; At01-2; At03; At05; At07; At08; At11; At14; At16; At18; At19; At20; At22; At24; At27; At32; FLO11; fungal invasion; secondary metabolite; At279; At286; At291; At320; At322; An1000; At117; At221; At223; At239; At240; At274; Pcl001; lovF; lovE; lovastatin; Pcl804; acvA; penicillin; antifungal; gene; db. Unidentified.

XX WO200257456-A2.

XX 25-JUL-2002.

XX 24-DEC-2001; 2001WO-US49911.

XX 22-DEC-2000; 2000US-257431P.

XX (MIRC-) MICROBIA.

XX PI Cali BM, Madden KT, Milne TG, Zhang L, Silva JC, Trueheart J;

XX PI Holtzman D, Sherman A;

XX DR WPI; 2002-627368/67.

XX DR P-PSDD; A8P63100.

XX New isolated or recombinant gene, or purified protein, useful in regulating fungal gene expression of FLO11, lovF, lovE or acvA for the production of enzymes, secondary metabolites or other commercially and/or medicinally useful products. The genes may also be used to identify genes relevant to fungal invasion which may act as targets for the development of antifungal drugs.

PT medically useful products -
XX
PS Claim 1; Page 43-44; 71PP; English.

CC The present invention relates to novel fungal gene expression regulators

CC (AB94217-AB94285 and ABP6152). An01, An05, An10, An11,

CC An17, An20, An28, An34, At01-1, At01-2, At03, At05, At07, At08, At11,

CC At14, At16, At18, At19, At20, At22, At24, At27, At32, Pcl05, Pcl06, Pcl07,

CC Pcl09, Pcl10, Pcl18, Pcl23, Pcl24, Pcl25, Pcl33 and Pcl34 are FLO11 gene

CC expression regulators. FLO11 is required for fungal invasion and its

CC expression is believed to be regulated by factors that also modulate

CC secondary metabolite production. At279, At286, At291, At322,

CC An1000, At167, At21, At239, At249, At274, Pcl000 and Pcl001 are

CC lovF gene expression regulators, and At250, and At274 are lovE gene

CC expression regulators. lovF and lovE are believed to be involved in the

CC production of the secondary metabolite lovastatin. Pcl804 is an acvA gene

CC expression regulator. acvA is involved in the production of the secondary

CC metabolite penicillin. The fungal gene expression regulators and their

CC coding sequences are useful in regulating or manipulating the expression

CC of fungal genes that are involved in the production of enzymes, secondary

CC metabolites and other commercially and medically useful products, in

CC order to achieve maximum benefit. The genes may also be used to identify

CC genes relevant to fungal invasion which may act as targets for the

CC development of antifungal drugs.

XX Sequence 3645 BP; 948 A; 1237 C; 933 G; 527 T; 0 other;

XX SQ Query Match 82.9%; Score 17.4; DB 24; Length 3645;

XX Best Local Similarity 94.7%; Pred. No. 3.8e+02;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Qy 2 CTGGCGGAGTGGGGCC 20

DB 2566 CTGGCGGAGATGGGGCC 2548

XX RESULT 13

XX ID ABQ94271c

XX ID ABQ94271 standard; DNA; 3732 BP.

XX XX AC ABQ94271;

XX DT 22-OCT-2002 (first entry)

XX XX DT 22-OCT-2002 (first entry)

XX XX Fungal gene expression regulator coding sequence SEQ ID 109.

XX Fungal gene expression regulator; fungicide; gene therapy; An01; An05;

XX An07; At08; At11; At14; At16; At18; At19; At20; At22; At24; At27; At32;

XX FLO11; fungal invasion; secondary metabolite; At279; At286; At291; At320;

XX At322; An1000; At117; At221; At223; At239; At240; At274; Pcl001; lovF;

XX lovE; lovastatin; Pcl804; acvA; penicillin; antifungal; gene; db.

XX Unidentified.

XX OS WO200257456-A2.

XX XX PN WO200257456-A2.

XX XX PD 25-JUL-2002.

XX XX PP 24-DEC-2001; 2001WO-US49911.

XX XX PP 24-DEC-2001; 2001WO-US49911.

XX XX PR 22-DEC-2000; 2000US-257431P.

XX XX PA (MIRC-) MICROBIA.

XX XX PI Cali BM, Madden KT, Milne TG, Zhang L, Silva JC, Trueheart J;

XX PI Holtzman D, Sherman A;

XX DR WPI; 2002-627368/67.

XX DR P-PSDD; A8P63100.

XX New isolated or recombinant gene, or purified protein, useful in

PT regulating fungal gene expression of FLO11, lovF, lovE or acvA for the

PT regulating fungal gene expression of FLO11, lovF, lovE or acvA for the

production of enzymes, secondary metabolites or other commercially and medicinally useful products

Disclosure: Page 63-64; 71pp; English.

CC The present invention relates to novel fungal gene expression regulators (ABQ94217, ABQ94285 and ABP63152). An01, An05, An09, An10, An13, An17, An20, An28, An34, At01-2, At03, At05, At07, At08, At11, At14, At16, At18, At19, At20, At22, At24, At27, At32, Pco6, Pco7, Pco8, Pco9, Pco10, Pcl8, Pc18, Pc23, Pc25, Pc33 and Pc34 are FLO11 gene expression regulators. FLO11 is required for fungal invasion and its expression is believed to be regulated by factors that also modulate secondary metabolite production. At279, At286, At291, At320, At322, An100, At167, At221, At233, At239, At240, At274, Pcl000 and Pcl001 are lovF gene expression regulators, and At501 and At574 are lovB gene expression regulators. lovF and lovB are believed to be involved in the production of the secondary metabolite lovastatin. Pcl004 is an actA gene expression regulator. actA is involved in the production of the secondary metabolite penicillin. The fungal gene expression regulators and their coding sequences are useful in regulating or manipulating the expression of fungal genes that are involved in the production of enzymes, secondary metabolites and other commercially and medicinally useful products, in order to achieve maximum benefit. The genes may also be used to identify genes relevant to fungal invasion which may act as targets for the development of antifungal drugs.

XX Sequence 3732 BP; 969 A; 1265 C; 951 G; 547 T; 0 other;

Query Match 82.9%; Score 17.4%; DB 24; Length 3732;

Best Local Similarity 94.7%; Pred. No. 3. 8e+02; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1;

Qy 2 CTGGCGGAACTTGGGGCC 20

Db 2566 CTGGCGGGAGATGGGGCC 2548

Query Match 82.9%; Score 17.4%; DB 24; Length 3732;

Best Local Similarity 94.7%; Pred. No. 3. 8e+02; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1;

Qy 2 CTGGCGGAACTTGGGGCC 20

Db 2566 CTGGCGGGAGATGGGGCC 2548

RESULT 14
ID ABZ57220 standard; cDNA; 2137 BP.

XX AC ABZ57220;

XX DT 24-MAR-2003 (first entry)

XX Human zinc finger protein 11.22-encoding cDNA.

XX Human; zinc finger protein 11.22; recombinant production;

XX gene therapy; malignant tumour; cancer; blood disease; HIV infection;

XX human immunodeficiency virus; immune disorder; inflammatory condition;

XX cytosatic; antiinflammatory; immunomodulator; gene; ss.

XX Homo sapiens.

XX Key CDS Location/Qualifiers

XX 6..314

XX /*tag= a /product= "Human zinc finger protein 11.22"

XX CN1364797-A.

XX 21-AUG-2002.

XX 10-JAN-2001; 2001CN-0105174.

XX 10-JAN-2001; 2001CN-0105174.

XX (BIOW-) BIOWINOW GENE DEV INC SHANGHAI.

XX PA 21-AUG-2002.

XX PR 10-JAN-2001; 2001CN-0105174.

XX PR 10-JAN-2001; 2001CN-0105174.

XX PA CN1364797-A.

XX 21-AUG-2002.

XX PR 10-JAN-2001; 2001CN-0105174.

XX PR 10-JAN-2001; 2001CN-0105174.

XX PA (BIOW-) BIOWINOW GENE DEV INC SHANGHAI.

XX PI Mao Y, Xie Y;

XX DR 2003-000509/01.

DR (PSDB; ABP58706.

XX PT New polypeptide-human zinc finger protein 11.22 and polynucleotide PT encoding for the polypeptide, useful for treating various diseases such PT as malignant tumors, hemopathy, HIV infection, immunological diseases XX and inflammation -

XX PS Claim 6; Page 25-26 (Disclosure); 33pp; Chinese.

XX CC The invention relates to human zinc finger protein 11.22 (ABP58706) and CC nucleic acids encoding it (ABZ57220). The protein has a molecular weight CC of 11.22 kD. The invention also relates to a method for the recombinant CC production of the protein, an antagonist of the protein, and the use of CC the protein, gene and antagonist in therapeutic applications. Zinc finger CC protein 11.22 can be used in the treatment of a variety of diseases such CC as malignant tumours, blood diseases, HIV (human immunodeficiency virus) CC infection, immune disorders and inflammatory conditions. The present CC sequence represents cDNA encoding human zinc finger protein 11.22.

XX SQ Sequence 2137 BP; 591 A; 487 C; 469 G; 590 T; 0 other;

Query Match 80.0%; Score 16.8; DB 25; Length 2137;

Best Local Similarity 90.0%; Pred. No. 6. 7e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGACTTGGGGCC 20

Db 762 GCTGGGGGGGGGGGGGG 781

XX DT 22-AUG-2001 (first entry)

XX ID AAH25134 standard; DNA; 2535 BP.

XX AC AAH25134;

XX DT 22-AUG-2001 (first entry)

XX DE Nucleotide sequence of human alcohol dehydrogenase 21612.

XX KW Human; alcohol dehydrogenase; colon disorder; brain disorder; kidney disorder; skin disorder; heart disorder; blood vessel disorder; prostate disorder; KW skeletal muscle disorder; ovarian disorder; testis disorder; KW liver disorder; epididymis disorder; spleen disorder; lung disorder; KW red cell disorder; endometrium disorder; T-cell disorder; KW thyroid disorder; thymus disorder; B cell disorder; breast disorder; KW reduced platelet number disorder; precursor T cell neoplasm; ss. XX Homo sapiens.

XX FH 762..2018

XX Key CDS /tag= a /product= "alcohol dehydrogenase 21612"

XX FT FT

XX PN WO200144446-A2.

XX PD 21-JUN-2001.

XX PR 15-DEC-2000; 2000WO-US33873.

XX PR 15-DEC-1999; 99US-0464039.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Meyers R;

XX DR WPI; 2001-390244/41.

XX DR P-PSDB; AAB84367.

XX PT Novel human alcohol dehydrogenase proteins, 21612, 21615, 21620, 21676, goiter, osteomalacia, endometriosis, angina pectoris, embolism -

XX Claim 2; Fig 15; 156pp; English.

PS
XX
AAH25131-35 encode human alcohol dehydrogenase proteins, designated
CC 21620, 33756, 21576, 21612 and 21615, respectively. Alcohol dehydrogenase
CC polynucleotides and polypeptides are useful for treatment and diagnosis
CC of disorders mediated by or related to alcohol dehydrogenase. They can
CC be used for treating disorders of colon, brain, skin, heart, blood
vessels, kidney, prostate, skeletal muscle, ovary, testis and epididymis,
CC spleen, lung, liver, uterus and endometrium, T-cells, red cells, thymus,
CC B cells, breast, thyroid, pancreas, small intestine, reduced platelet
CC number, precursor T cell neoplasms, bone forming cells, and bone marrow
CC cells.

XX Sequence 2535 BP; 720 A; 531 C; 537 G; 695 T; 52 other;

SQ Query Match 80.0%; Score 16.8; DB 22; Length 2535;

Best Local Similarity 90.0%; Pred. No. 6.7e+02; Matches 18; Conserv. 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGGGGGAGTGGGGCC 20
Db 73 GATGGGGAGTTAGGGCC 54

Search completed: January 21, 2004, 11:44:48
Job time : 151 secs

This Page Blank (uspto)

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw mode!

Run on: January 21, 2004, 12:11:53 ; Search time 217 Seconds
 (without alignments)

341.106 Million cell. updates/sec

Title: US-09-913-325-12

Perfect score: 21

Sequence: 1 gctggcgaggatgtggggcct 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2324096 seqs, 1762381658 residues

Total number of hits satisfying chosen parameters: 4648192

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/_ptodata/2/pubnpa/US07_PUBCOMB.seq:*

2: /cgn2_6/_ptodata/2/pubnpa/PCT_NEW_PUB.seq:*

3: /cgn2_6/_ptodata/2/pubnpa/US06_NEW_PUB.seq:*

4: /cgn2_6/_ptodata/2/pubnpa/US05_PUBCOMB.seq:*

5: /cgn2_6/_ptodata/2/pubnpa/US04_PUBCOMB.seq:*

6: /cgn2_6/_ptodata/2/pubnpa/PCRT_PUBCOMB.seq:*

7: /cgn2_6/_ptodata/2/pubnpa/US07_NEW_PUB.seq:*

8: /cgn2_6/_ptodata/2/pubnpa/US09A_PUBCOMB.seq:*

9: /cgn2_6/_ptodata/2/pubnpa/US06_PUBCOMB.seq:*

10: /cgn2_6/_ptodata/2/pubnpa/US05_PUBCOMB.seq:*

11: /cgn2_6/_ptodata/2/pubnpa/US04_PUBCOMB.seq:*

12: /cgn2_6/_ptodata/2/pubnpa/US09_NEW_PUB.seq:*

13: /cgn2_6/_ptodata/2/pubnpa/US09_NEW_PUB.seq:*

14: /cgn2_6/_ptodata/2/pubnpa/US10_PUBCOMB.seq:*

15: /cgn2_6/_ptodata/2/pubnpa/US10_PUBCOMB.seq:*

16: /cgn2_6/_ptodata/2/pubnpa/US60_NEW_PUB.seq:*

17: /cgn2_6/_ptodata/2/pubnpa/US60_PUBCOMB.seq:*

18: /cgn2_6/_ptodata/2/pubnpa/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	21	100.0	21	10 US-09-944-326-12	Sequence 12, App1
2	21	100.0	21	13 US-09-947-726A-12	Sequence 12, App1
3	21	100.0	21	13 US-10-080-794-12	Sequence 12, App1
c 4	21	100.0	450	11 US-09-948-995-759	Sequence 759, App1
c 5	21	100.0	505	10 US-09-833-381-159	Sequence 159, App1
c 6	21	100.0	1495	13 US-10-210-120-74	Sequence 74, App1
c 7	21	100.0	1678	10 US-19-76-231A-16	Sequence 1678, App1
c 8	21	100.0	1775	13 US-10-133-013-243	Sequence 1775, App1
c 9	21	100.0	2876	15 US-10-116-255-17	Sequence 17, App1
c 10	21	100.0	3196	10 US-19-965-708-160	Sequence 160, App1
c 11	21	100.0	3196	13 US-19-833-367C-71	Sequence 16, App1
c 12	19.4	92.4	403	10 US-09-833-381-444	Sequence 444, App1
c 13	19.4	92.4	525	10 US-09-833-381-443	Sequence 443, App1
c 14	19.4	92.4	4283	13 US-09-834-353-1951	Sequence 15011, App1
c 15	18.4	87.6	2257	13 US-10-027-632-101667	Sequence 101667, App1

ALIGNMENTS

RESULT 1	Sequence 12, Application US/09944326
	Patent No. US20020128220A1
	GENERAL INFORMATION:
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Nelson, Colleen
	APPLICANT: Riede, Peter
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter
	APPLICANT: Nelson, Colleen
	APPLICANT: Gleave, Martin S.
	APPLICANT: Gleave, Martin S.
	APPLICANT: Reunie, Paul S.
	APPLICANT: Miyake, Hideaki
	APPLICANT: Riede, Peter

Sequence 12, Application US/0967726A
 Publication No. US20030158130A1
 GENERAL INFORMATION:
 APPLICANT: Gleave, Martin
 APPLICANT: Reunie, Paul S.
 APPLICANT: Miyake, Hideaki
 APPLICANT: Nelson, Colleen
 APPLICANT: Zellweger, Tobias
 TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
 TITLE OF INVENTION: Oligonucleotides
 FILE REFERENCE: UBC_P-022
 CURRENT APPLICATION NUMBER: US/09/967,726A
 CURRENT FILING DATE: 2001-09-28
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 12
 LENGTH: 21
 TYPE: DNA
 ORGANISM: human
 US-09-967-726A-12

Query Match 100.0%; Score 21; DB 13; Length 21;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTGGCGAGTGGGGCT 21
 Db 1 GCTGGCGAGTGGGGCT 21

RESULT 3
 US-10-080-794-12
 Sequence 12, Application US/10080794
 Publication No. US20030166591A1
 GENERAL INFORMATION:
 APPLICANT: Gleave, Martin
 APPLICANT: Reunie, Paul S.
 APPLICANT: Miyake, Hideaki
 APPLICANT: Nelson, Colleen
 APPLICANT: Monia, Brett P.
 TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
 FILE REFERENCE: UBC_P-020-3
 CURRENT APPLICATION NUMBER: US/10/080,794
 CURRENT FILING DATE: 2002-02-22
 PRIOR APPLICATION NUMBER: 60/121,726
 PRIOR FILING DATE: 1999-02-26
 PRIOR APPLICATION NUMBER: 09/913,325
 PRIOR FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: 09/944,326
 PRIOR FILING DATE: 2001-08-30
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 12
 LENGTH: 21
 TYPE: DNA
 ORGANISM: HUMAN
 FEATURE:
 OTHER INFORMATION: antisense TRPM-2 ODN
 US-10-080-794-12

Query Match 100.0%; Score 21; DB 13; Length 21;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTGGCGAGTGGGGCT 21
 Db 1 GCTGGCGAGTGGGGCT 21

RESULT 4
 US-09-918-995-759/c
 Sequence 759, Application US/09918995

Publication No. US20030073623A1
 GENERAL INFORMATION:
 APPLICANT: Hyseg, Inc.
 TITLE OF INVENTION: NOVEL NUCLEAR ACID SEQUENCES OBTAINED FROM VARIOUS CDNA LIBRARIES
 FILE REFERENCE: 20411-756
 CURRENT APPLICATION NUMBER: US/09/918,995
 CURRENT FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: US/09/235,076
 PRIOR FILING DATE: 1999-01-20
 NUMBER OF SEQ ID NOS: 3,8054
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 759
 LENGTH: 450
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(450)
 OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-759

RESULT 5
 US-09-833-381-159
 Sequence 159, Application US/098333381
 Publication No. US20030132090A1
 GENERAL INFORMATION:
 APPLICANT: Robison, Keith E.
 TITLE OF INVENTION: No. US20020132090A1 Nucleic Acid and Protein Homologs
 FILE REFERENCE: 5800-119
 CURRENT APPLICATION NUMBER: US/09/833,381
 CURRENT FILING DATE: 2001-04-11
 PRIOR APPLICATION NUMBER: US/09/516,448
 PRIOR FILING DATE: 2000-02-29
 NUMBER OF SEQ ID NOS: 2050
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 159
 LENGTH: 505
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-833-381-159

Query Match 100.0%; Score 21; DB 10; Length 505;
 Best Local Similarity 100.0%; Pred. No. 5,4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTGGCGAGTGGGGCT 21
 Db 105 GCTGGCGAGTGGGGCT 125

RESULT 6
 US-10-2-120-74/c
 Sequence 74, Application US/10210120
 Publication No. US20030175736A1
 GENERAL INFORMATION:
 APPLICANT: Chinaiyan, Arul M.
 APPLICANT: Rubin, Mark A.
 APPLICANT: Sreekumar, Arun
 TITLE OF INVENTION: Expression Profile of Prostate Cancer
 FILE REFERENCE: US-07221
 CURRENT APPLICATION NUMBER: US/10/210,120
 CURRENT FILING DATE: 2002-08-01
 PRIOR APPLICATION NUMBER: US 60/309,541

PRIOR FILING DATE: 2001-08-02
 PRIOR APPLICATION NUMBER: US 60/334,468
 PRIOR FILING DATE: 2001-11-15
 NUMBER OF SEQ ID NOS: 123
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 74
 LENGTH: 1495
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-765-231A-16

Query Match 100.0%; Score 21; DB 13; Length 1495;

Best Local Similarity 100.0%; Pred. No. 4,4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGGGAGGTGGGGCT 21
 Db 1388 GCTGGGGAGGTGGGGCT 1368

RESULT 7
 US-09-765-231A-16/C

Sequence 16, Application US/09765231A
 Patent No. US2002119452A1

GENERAL INFORMATION:

APPLICANT: Searle/Monsanto

ASSIGNEE: Philippard, Deborah

APPLICANT: Vasanthakumar, Geerha

APPLICANT: Dorson, Stanton

APPLICANT: Ma, Xiao-Jun

TITLE OF INVENTION: Osteoarthritis tissue-derived nucleic acids, polypeptides,

TITLE OF INVENTION: vectors, and cells

FILE REFERENCE: SO-3221 PR

CURRENT APPLICATION NUMBER: US/09/765.231A

CURRENT FILING DATE: 2001-01-18

NUMBER OF SEQ ID NOS: 82

SEQ ID NO: 16

LENGTH: 1678

TYPE: DNA

ORGANISM: Homo sapiens

US-09-765-231A-16

Query Match 100.0%; Score 21; DB 13; Length 1775;

Best Local Similarity 100.0%; Pred. No. 4,2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGGGAGGTGGGGCT 21
 Db 1650 GCTGGGGAGGTGGGGCT 1650

RESULT 9
 US-10-116-255-17/C

Sequence 17, Application US/10116255
 Patent No. US2003036664A1

GENERAL INFORMATION:

APPLICANT: Ni et al.

TITLE OF INVENTION: Uncoupling Protein Polynucleotides, Polypeptides, and

FILE REFERENCE: PT009P1

CURRENT APPLICATION NUMBER: US/10/116,255

CURRENT FILING DATE: 2002-04-05

PRIOR APPLICATION NUMBER: 09/685,897

PRIOR FILING DATE: 2000-10-11

PRIOR APPLICATION NUMBER: PCT/US00/09534

PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: 60/128,701

PRIOR FILING DATE: 1999-04-09

PRIOR APPLICATION NUMBER: 60/142,821

PRIOR FILING DATE: 1999-07-08

PRIOR APPLICATION NUMBER: 60/149,448

PRIOR FILING DATE: 1999-08-18

PRIOR APPLICATION NUMBER: 60/164,751

PRIOR FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 17

LENGTH: 2876

TYPE: DNA

ORGANISM: Homo sapiens

US-10-116-255-17

Query Match 100.0%; Score 21; DB 15; Length 2876;

Best Local Similarity 100.0%; Pred. No. 3,8;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGGGAGGTGGGGCT 21
 Db 2734 GCTGGGGAGGTGGGGCT 2714

RESULT 10
 US-09-969-708-160/C

Sequence 160, Application US/09969708
 Patent No. US2002010252A1

GENERAL INFORMATION:

APPLICANT: Augustus, Meena

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu

FILE REFERENCE: 689290-70

CURRENT APPLICATION NUMBER: US/09/959,708

CURRENT FILING DATE: 2001-10-03

PRIOR APPLICATION NUMBER: US/60/237,606

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: US/60/237,608

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: US/60/237,425

PRIOR FILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 658

SOFTWARE: PatentIn Ver. 3.0

SEQ ID NO: 160

LENGTH: 3196

RESULT 8
 US-10-133-013-243/C

Sequence 243, Application US/10133013
 Publication No. US20030166903A1

GENERAL INFORMATION:

APPLICANT: Astromoff, Anna

ASSIGNEE: Bandman, Olga

APPLICANT: Cocks, Benjamin G.

TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE

FILE REFERENCE: PA-0049 US

CURRENT APPLICATION NUMBER: US/10/133,013

CURRENT FILING DATE: 2002-04-25

PRIOR APPLICATION NUMBER: 60/287,067

NUMBER OF SEQ ID NOS: 271

SOFTWARE: PERL Program

SEQ ID NO: 243

LENGTH: 1775

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: misc_feature

NAME/KEY: misc_feature

1 TYPE: DNA ORGANISM: Homo sapiens
 US-09-969-708-160

Query Match 100.0%; Score 21; DB 10; Length 3196;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCT 21
 Db 2891 GCTGGCGGAGTTGGGGCCT 2871

RESULT 13
 US-09-833-381-443
 ; Sequence 443, Application US/09833381
 ; Patent No. US2002132050A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Robison, Keith E.
 ; TITLE OF INVENTION: US/0920132050A1 Nucleic Acid and Protein Homologs
 ; FILE REFERENCE: 5800-119
 ; CURRENT APPLICATION NUMBER: US/09/833,381
 ; CURRENT FILING DATE: 2001-04-11
 ; PRIOR APPLICATION NUMBER: 09/516,448
 ; PRIOR FILING DATE: 2000-02-29
 ; NUMBER OF SEQ ID NOS: 2050
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 443
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-833-381-443

Query Match 92.4%; Score 19.4; DB 10; Length 403;
 Best Local Similarity 95.2%; Pred. No. 27;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCT 21
 Db 102 GCTGGCGGAGTTGGGGCCT 122

RESULT 14
 US-09-814-353-19511/c
 ; Sequence 19511, Application US/09814353
 ; Publication No. US2003165831A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lee, John
 ; APPLICANT: Thompson, Pamela
 ; APPLICANT: Lillie, James
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
 ; FILE REFERENCE: MRI-006B
 ; CURRENT APPLICATION NUMBER: US/09/814,353
 ; CURRENT FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: US 60/191,031
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: US 60/207,124
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: US 60/211,940
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: US 60/216,820
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: US 60/220,661
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: US 60/257,672
 ; PRIOR FILING DATE: 2000-12-21
 ; NUMBER OF SEQ ID NOS: 22037
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 19511
 ; LENGTH: 4283
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-814-353-19511

Query Match 100.0%; Score 21; DB 13; Length 3196;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCGGAGTTGGGGCCT 21
 Db 2891 GCTGGCGGAGTTGGGGCCT 2871

RESULT 15
 US-09-833-381-444
 ; Sequence 444, Application US/09833381
 ; Patent No. US2002132050A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Robison, Keith E.
 ; TITLE OF INVENTION: US/0920132050A1 Nucleic Acid and Protein Homologs
 ; FILE REFERENCE: 5800-119
 ; CURRENT APPLICATION NUMBER: US/09/833,381
 ; CURRENT FILING DATE: 2001-04-11
 ; PRIOR APPLICATION NUMBER: 09/516,448
 ; PRIOR FILING DATE: 2000-02-29
 ; NUMBER OF SEQ ID NOS: 2050
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 444
 ; LENGTH: 403
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-833-381-444

```

Query Match      92.4%;  Score 19.4;  DB 13;  Length 4283;
Best Local Similarity 95.2%;  Pred. No. 17;
Matches 20;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;
Qy      1 GCTGGGGAGATTGGGGCT 21
Db      1490 GCTGGGGAGATTGGGGCT 1470

```

```

RESULT 15
US10-027-632-101667
Sequence 101667, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 101667
LENGTH: 2257
TYPE: DNA
ORGANISM: Human
US-10-027-632-101667

```

```

Query Match      87.6%;  Score 18.4;  DB 13;  Length 2257;
Best Local Similarity 95.0%;  Pred. No. 50;
Matches 19;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;
Qy      2 CTCGGGGAGATTGGGGCT 21
Db      1340 CTCGGGGAGATTGGGGCT 1359

```

Search completed: January 21, 2004, 15:35:50
 Job time : 224 secs

This Page Blank (uspto)

Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 11:34:17 ; Search time 56 Seconds

(without alignments)
165,519 Million cell updates/sec

Title: US-09-913-325-12

Perfect score: 21

Sequence: 1 gctggcgagtcggggct 21

Scoring table: IDENTITY NUC

Gapop 10- , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first: 45 summaries

Database : Issued_Patents_NA:
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfile1.seq:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
C 1	21	100.0	1416	4	US-09-016-434-1318		Sequence 1318, App
C 2	21	100.0	1648	4	US-09-065-79A-3		Sequence 3, App
C 3	21	100.0	8133	4	US-09-065-79A-10		Sequence 10, App
C 4	16.8	80.0	3562	3	US-09-366-197-1		Sequence 1, App
C 5	16.8	80.0	3647	3	US-09-366-197-1		Sequence 7, App
C 6	16.4	78.1	50	1	US-08-171-389-590		Sequence 590, App
C 7	16.4	78.1	50	1	US-08-122-936-590		Sequence 590, App
C 8	16.4	78.1	50	1	US-08-475-22A-590		Sequence 590, App
C 9	16.4	78.1	50	3	US-08-482-080A-590		Sequence 590, App
C 10	16.4	78.1	50	4	US-09-354-947-590		Sequence 590, App
C 11	16.4	78.1	50	5	PCT-US93-12389-590		Sequence 590, App
C 12	16.4	78.1	68	3	US-08-196-963-66		Sequence 66, App
C 13	16.4	78.1	50	1	US-09-371-774-66		Sequence 66, App
C 14	16.4	78.1	226	4	US-09-065-026A-9		Sequence 9, App
C 15	16.4	78.1	256	3	US-09-101-182-24		Sequence 24, App
C 16	16.4	78.1	256	4	US-09-222-357-10		Sequence 10, App
C 17	16.4	78.1	256	4	US-09-280-839-13		Sequence 13, App
C 18	16.4	78.1	256	4	US-09-411-977-24		Sequence 24, App
C 19	16.4	78.1	256	4	US-09-477-729B-30		Sequence 30, App
C 20	16.4	78.1	256	4	US-09-257-179-10		Sequence 10, App
C 21	16.4	78.1	256	4	US-09-147-476-10		Sequence 10, App
C 22	16.4	78.1	256	4	US-09-288-143-10		Sequence 10, App
C 23	16.4	78.1	256	4	US-09-487-792-32		Sequence 32, App
C 24	16.4	78.1	256	4	US-09-156-060-10		Sequence 10, App
C 25	16.4	78.1	256	4	US-09-905-594-32		Sequence 32, App
C 26	16.4	78.1	256	4	US-09-461-325-10		Sequence 10, App
C 27	16.4	78.1	256	4	US-09-489-847-10		Sequence 10, App

ALIGNMENTS

C 28	16.4	78.1	256	4	US-09-231-788-26	Sequence 26, App
C 29	16.4	78.1	256	4	US-09-512-363-27	Sequence 27, App
C 30	16.4	78.1	256	4	US-09-176-200-27	Sequence 27, App
C 31	16.4	78.1	256	4	US-09-205-258-10	Sequence 27, App
C 32	16.4	78.1	256	4	US-09-690-454-10	Sequence 10, App
C 33	16.4	78.1	256	4	US-09-482-271-19	Sequence 10, App
C 34	16.4	78.1	256	4	US-09-482-273-10	Sequence 10, App
C 35	16.4	78.1	256	4	US-09-904-151-10	Sequence 10, App
C 36	16.4	78.1	256	4	US-09-369-247-10	Sequence 10, App
C 37	16.4	78.1	271	3	US-09-106-182-18	Sequence 18, App
C 38	16.4	78.1	271	4	US-09-227-357-5	Sequence 5, App
C 39	16.4	78.1	271	4	US-09-280-839-8	Sequence 8, App
C 40	16.4	78.1	271	4	US-09-411-977-20	Sequence 20, App
C 41	16.4	78.1	271	4	US-09-479-729B-25	Sequence 25, App
C 42	16.4	78.1	271	4	US-09-149-476-5	Sequence 5, App
C 43	16.4	78.1	271	4	US-09-288-143-5	Sequence 5, App
C 44	16.4	78.1	271	4	US-09-487-792-27	Sequence 27, App

RESULTS

RESULT 1	US-09-016-434-1318/c	Computer readable form:
	Sequence 1318, Application US/09016434	Medium type: floppy disk
	Parent No. 650093B	Computer: IBM PC compatible
	GENERAL INFORMATION:	Operating system: PC-DOSS/MS-DOS
	APPLICANT: Janice Au Young	Software: Word Perfect 6.1 for windows/MS-DOS
	TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING	CURRENT APPLICATION DATA:
	NUMBER OF SEQUENCES: 1490	APPLICATION NUMBER: US/09/016,434
	CORRESPONDENCE ADDRESS:	FILING DATE: HEREBWITH
	ADDRESSEE: INCYTE PHARMACEUTICALS, INC.	CLASSIFICATION:
	STREET: 3174 PORTER DRIVE	PRIOR APPLICATION DATA:
	CITY: PALO ALTO	APPLICATION NUMBER:
	STATE: CALIFORNIA	OPERATING CHARACTERISTICS:
	COUNTRY: USA	TELECOMMUNICATION:
	ZIP: 94304	CLASSIFICATION:
	ATTORNEY/AGENT INFORMATION:	TELEPHONE: (650) 855-0555
	NAME: Zeller, Karen J.	FAX: (650) 845-4166
	REGISTRATION NUMBER: 37,071	INFORMATION FOR SEQ ID NO: 1318:
	REFERENCE/DOCKET NUMBER: PA-0002 US	SEQUENCE CHARACTERISTICS:
	TELECOMMUNICATION:	LENGTH: 1416 base pairs
	CLASSIFICATION:	TYPE: nucleic acid
	TELEPHONE: (650) 855-0555	STRANDEDNESS: single
	IMMEDIATE SOURCE:	TOPOLOGY: linear
	LIBRARY: GENBANK	SEQUENCE: 1318
	CLONE: 9333056	VERSION: 1
	US-09-016-434-1318	LENGTH: 1416;
	Query Match Similarity 100.0%	Score 21; DB 4; Pred. No. 2.1;
	Best Local Similarity 100.0%	Score 10; App

RESULT 2
US-09-659-791A-3/c
Sequence 3, Application US/09659791A
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
PATENT NO. 6383808
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
FILE REFERENCE: RTS-0156
CURRENT APPLICATION NUMBER: US/09/659,791A
CURRENT FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 3
LENGTH: 1648
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (53) . . . (1402)
US-09-659-791A-3.

Query Match 100.0%; Score 21; DB 4; Length 1648;
Best Local Similarity 100.0%; Pred. No. 2.1; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-659-791A-10/c
Sequence 10, Application US/09659791A
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
PATENT NO. 6383808
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
FILE REFERENCE: RTS-0156
CURRENT APPLICATION NUMBER: US/09/659,791A
CURRENT FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 10
LENGTH: 8133
TYPE: DNA
ORGANISM: Homo sapiens
US-09-659-791A-10

Query Match 100.0%; Score 21; DB 4; Length 8133;
Best Local Similarity 100.0%; Pred. No. 2.2; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-09-659-791A-10/c
Sequence 1, Application US/09659791A
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
PATENT NO. 6287159
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
FILE REFERENCE: RTS-0156
CURRENT APPLICATION NUMBER: US/09/659,791A
CURRENT FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 1
LENGTH: 8133
TYPE: DNA
ORGANISM: Homo sapiens
US-09-659-791A-10

Query Match 100.0%; Score 21; DB 4; Length 8133;
Best Local Similarity 100.0%; Pred. No. 2.2; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-09-360-197-1/c
Sequence 1, Application US/09360197
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
PATENT NO. 6287159
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
FILE REFERENCE: RTS-0156
CURRENT APPLICATION NUMBER: US/09/360,197
CURRENT FILING DATE: 1997-07-23
PRIORITY NUMBER: 09/129,758
PRIORITY FILING DATE: 1998-08-05
PRIORITY APPLICATION NUMBER: 60/095,408
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 3562
TYPE: DNA
ORGANISM: rattus sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (123) . . . (1700)
US-09-360-197-1

Query Match 80.0%; Score 16.8; DB 3; Length 3562;
Best Local Similarity 90.0%; Pred. No. 1.1e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 18; Conservative 0;

Qy 1 GCTGGGGGAGTGGGGCC 20
Db 1778 GCTGGGGCAGTGGGGGCC 1759

RESULT 5
US-09-360-197-7/c
Sequence 7, Application US/09360197
PATENT NO. 6287159
GENERAL INFORMATION:
APPLICANT: Bassilana, Frederic
APPLICANT: Lazdunski, Michel
APPLICANT: Waldmann, Rainer
APPLICANT: Dewelle, Jan R.
TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive Cationic Channels, Their Cloning and Applications
FILE REFERENCE: 989 6706P
CURRENT APPLICATION NUMBER: US/09/360,197
CURRENT FILING DATE: 1997-07-23
PRIORITY NUMBER: 09/129,758
PRIORITY FILING DATE: 1998-08-05
PRIORITY APPLICATION NUMBER: 60/095,408
PRIORITY FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 3647
TYPE: DNA
ORGANISM: rattus sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (109) . . . (1785)
US-09-360-197-7

Query Match 80.0%; Score 16.8; DB 3; Length 3647;
Best Local Similarity 90.0%; Pred. No. 1.1e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 18; Conservative 0;

Qy 1 GCTGGGGGAGTGGGGCC 20
Db 1863 GCTGGGGCAGTGGGGGCC 1844

RESULT 6
US-08-171-389-590/c
Sequence 590, Application US/08171389
GENERAL INFORMATION:
PATENT NO. 5518444
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: DeWeille, Jan R.
APPLICANT: Bassilana, Frederic
APPLICANT: Lazdunski, Michel
APPLICANT: Waldmann, Rainer
APPLICANT: Dewelle, Jan R.

APPLICANT: Cantor, Charles R.
 APPLICANT: Andrews, Beth M.
 APPLICANT: Turin, Lisa M.
 APPLICANT: Fry, Kirk E.
 TITLE OF INVENTION: Sequence-Directed DNA Binding Molecules, Compositions and Methods
 NUMBER OF SEQUENCES: 641
 CORRESPONDENCE ADDRESS:
 ADDRESS: Genelabs Technologies, Inc.
 STREET: 505 Penobscot Drive
 CITY: Redwood City
 STATE: CA
 COUNTRY: USA
 ZIP: 94063
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/171,389
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/123,936
 FILING DATE: 17-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/996,783
 FILING DATE: 23-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/723,618
 FILING DATE: 27-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/997,543
 FILING DATE: 22-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/081,070
 FILING DATE: 22-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 4600-0175/G19B3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 590:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 50 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start site 31)
 INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start site 31)
 US-08-171-389-590

Query Match 78.1%; Score 16.4; DB 1; Length 50;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGGGGAGGTGGGGC 19
 Db 20 CTGGGGGAGTTAGGGC 3

RESULT 7
 US-08-123-936-590/c
 Sequence 590, Application US/08123936
 Patent No. 572604
 GENERAL INFORMATION:
 APPLICANT: Edwards, Cynthia A.
 APPLICANT: Cantor, Charles R.
 APPLICANT: Andrews, Beth M.
 APPLICANT: Turin, Lisa M.

TITLE OF INVENTION: Sequence-Directed DNA Binding Molecules, Compositions and Methods
 NUMBER OF SEQUENCES: 664
 CORRESPONDENCE ADDRESS:
 ADDRESS: Genelabs Technologies, Inc.
 STREET: 505 Penobscot Drive
 CITY: Redwood City
 STATE: CA
 COUNTRY: USA
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/123,936
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/996,783
 FILING DATE: 23-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/723,618
 FILING DATE: 27-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 4600-0075,32/G19P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 590:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 50 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start site 31)
 INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start site 31)
 US-08-123-936-590

Query Match 78.1%; Score 16.4; DB 1; Length 50;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGGGGAGGTGGGGC 19
 Db 20 CTGGGGGAGTTAGGGC 3

RESULT 8
 US-08-475-228A-590/c
 Sequence 590, Application US/08475228A
 Patent No. 5669241
 GENERAL INFORMATION:
 APPLICANT: Edwards, Cynthia A.
 APPLICANT: Cantor, Charles R.
 APPLICANT: Andrews, Beth M.
 APPLICANT: Turin, Lisa M.
 APPLICANT: Fry, Kirk E.
 TITLE OF INVENTION: Sequence-Directed DNA Binding Molecules, Compositions and Methods
 NUMBER OF SEQUENCES: 664
 CORRESPONDENCE ADDRESS:
 ADDRESS: Genelabs Technologies, Inc.
 STREET: 505 Penobscot Drive
 CITY: Redwood City
 STATE: CA
 COUNTRY: USA

ZIP: 94063
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/475,228A
 FILING DATE: 06-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/475,228A
 FILING DATE: 17-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/996,783
 FILING DATE: 23-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/123,936
 FILING DATE: 27-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/081,070
 FILING DATE: 24-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Stratford, Carol A.
 REGISTRATION NUMBER: 34,444
 REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0560
 INFORMATION FOR SEQ ID NO: 590:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 50 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
 INDIVIDUAL ISOLATE: site 31)
 US-08-475-228A-590

Query Match 78.1%; Score 16.4%; DB 3; Length 50;

Best Local Similarity 94.4%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGGGAGGTGGGGC 19
 Db 20 CTGGGGAGGTAGGGC 3

RESULT 9
 US-08-482-080A-590/C

/ Sequence 590, Application US/08482080A
 / General Information:
 / APPLICANT: Edwards, Cynthia A.

/ APPLICANT: Cantor, Charles R.
 / APPLICANT: Andrews, Beth M.
 / APPLICANT: Turin, Lisa M.

/ APPLICANT: Fry, Kirk E.
 / TITLE OF INVENTION: Sequence-Directed DNA Binding
 / TITLE OF INVENTION: Sequences-Directed DNA Binding
 / NUMBER OF SEQUENCES: 664
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: Genelabs Technologies, Inc.
 / STREET: 505 Penobscot Drive
 / CITY: Redwood City
 / STATE: CA
 / COUNTRY: USA
 / ZIP: 94063

/ COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / ZIP: 94063
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,080A
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/171,389
 FILING DATE: 20-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/123,936
 FILING DATE: 17-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/996,783
 FILING DATE: 23-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/723,618
 FILING DATE: 27-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/081,070
 FILING DATE: 22-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Brady, John F.
 REGISTRATION NUMBER: 39,118
 REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 324-0880
 TELEFAX: (650) 324-0900
 INFORMATION FOR SEQ ID NO: 590:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 50 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
 INDIVIDUAL ISOLATE: site 31)
 US-08-482-080A-590

Query Match 78.1%; Score 16.4%; DB 3; Length 50;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGGGAGGTGGGGC 19
 Db 20 CTGGGGAGGTAGGGC 3

RESULT 10
 US-09-354-947-590/C
 / Sequence 590, Application US/09354947
 / General Information:
 / APPLICANT: Edwards, Cynthia A.
 / APPLICANT: Cantor, Charles R.
 / APPLICANT: Andrews, Beth M.
 / APPLICANT: Turin, Lisa M.
 / APPLICANT: Fry, Kirk E.
 / TITLE OF INVENTION: Sequence-Directed DNA Binding
 / TITLE OF INVENTION: Molecules, Compositions and Methods
 / NUMBER OF SEQUENCES: 664
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: Genelabs Technologies, Inc.
 / STREET: 505 Penobscot Drive
 / CITY: Redwood City
 / STATE: CA
 / COUNTRY: USA
 / ZIP: 94063
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/354,947
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/482,080
 FILING DATE: 07-JUN-1995
 APPLICATION NUMBER: US 08/171,389
 FILING DATE: 20-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/123,936
 FILING DATE: 17-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/996,783
 FILING DATE: 23-DEC-1992
 APPLICATION NUMBER: US 07/996,783
 FILING DATE: 07/996,783
 APPLICATION NUMBER: US 08/081,070
 FILING DATE: 22-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Brady, John F.
 REGISTRATION NUMBER: 39,118
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 324-0960
 TELEXFAX: (650) 324-0960
 INFORMATION FOR SEQ ID NO: 590:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 50 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
 site 31)
 US-09-354-947-590

Query Match 78.1%; Score 16.4; DB 4; Length 50;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 CTGGGGAGGTGGGGC 19
 Db 20 CTGGGGAGGTAGGGC 3

RESULT 11
 PCT-US93-1238-590/c
 Sequence 590, Application PC/TUS9312388
 GENERAL INFORMATION:
 APPLICANT: Cooper & Dunham LLP
 TITLE OF INVENTION: Sequence-Directed DNA Bidding
 NUMBER OF SEQUENCES: 641
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GeneLabs Technologies, Inc.
 STREET: 505 Penobscot Drive
 CITY: Redwood City
 STATE: CA
 COUNTRY: USA
 ZIP: 94063
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/12388
 FILING DATE:

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 50130-B/JPW/ARC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEXFAX: 212-391-0326
 INFORMATION FOR SEQ ID NO: 66:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 68 base Pairs

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/123,936
 FILING DATE: 17-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/996,783
 FILING DATE: 23-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT12
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEXFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 590:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 50 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Simian virus 40 T/t late (start
 site 31)
 PCT-US93-12388-590

Query Match 78.1%; Score 16.4; DB 5; Length 50;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 CTGGGGAGGTGGGGC 19
 Db 20 CTGGGGAGGTAGGGC 3

RESULT 12
 US-08-790-963-66
 Sequence 66, Application US/08790963
 Parent No. 5837454
 GENERAL INFORMATION:
 APPLICANT: Daniel J. Capon
 ATTORNEY/AGENT INFORMATION:
 TITLE OF INVENTION: Compositions And Methods For
 Determining Anti-viral Drug Susceptibility And
 NUMBER OF SEQUENCES: 105
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/790,963
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 50130-B/JPW/ARC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEXFAX: 212-391-0326
 INFORMATION FOR SEQ ID NO: 66:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 68 base Pairs

TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

US-08-790-933-66

Query Match 13
 Best Local Similarity 94.4%; Score 16.4%; DB 2; Length 68;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SEQ ID NO: 9
 LENGTH: 226
 TYPE: DNA
 ORGANISM: IN VITROGEN
 US-09-659-026A-9

RESULT 13
 Sequence 66, Application US/09371774
 Patent No. 6,424,187
 GENERAL INFORMATION:
 APPLICANT: Daniel J. Capon
 Christos John Petropoulos
 TITLE OF INVENTION: Compositions And Methods For
 Determining Anti-viral Drug Susceptibility And
 Resistance and Anti-viral Drug Screening
 NUMBER OF SEQUENCES: 105
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version#1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/371,774
 FILING DATE: 10-Aug-1999
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 50130-F/JEW/CMR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0526
 INFORMATION FOR SEQ ID NO: 66:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 68 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 66:
 US-09-371-774-66

Query Match 14
 Best Local Similarity 94.4%; Score 16.4%; DB 3; Length 68;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SEQ ID NO: 11
 LENGTH: 226
 TYPE: DNA
 ORGANISM: IN VITROGEN
 US-09-659-026A-9

RESULT 14
 Sequence 9, Application US/09659026A
 Patent No. 6,461,616
 GENERAL INFORMATION:
 APPLICANT: MONTELARO, Ronald K.
 APPLICANT: CRAIGO, Jodi K.
 APPLICANT: ISSEL, Charlie
 APPLICANT: PUFFER, Bridget
 APPLICANT: HENNESSY, Kristina J.
 APPLICANT: BROWN, Karen K.
 TITLE OF INVENTION: EIAV P26 DELETION VACCINE AND DIAGNOSTIC
 FILE REFERENCE: MONTELARO ET AL.
 CURRENT APPLICATION NUMBER: US/09/659,026A
 CURRENT FILING DATE: 2001-06-11
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 9
 LENGTH: 226
 TYPE: DNA
 ORGANISM: IN VITROGEN
 US-09-659-026A-9

RESULT 15
 Sequence 24, Application US/09106182
 Patent No. 6,046,035
 GENERAL INFORMATION:
 APPLICANT: Shi, Yanggu
 APPLICANT: Rubin, Steve
 TITLE OF INVENTION: Cardiotrophin-Like Cytokine
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc
 STREET: 9410 Key West Ave
 CITY: Rockville
 STATE: MD
 COUNTRY: US
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/106,182
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/051,053
 FILING DATE: 30-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Brookes, A. Anders
 REGISTRATION NUMBER: 26,373
 REFERENCE/DOCKET NUMBER: PF385
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-309-8504
 TELEFAX: 301-309-8439
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 256 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 19
 Db 33 CTGGCGGAGTTAGGGC 50
 Db 33 CTGGCGGAGTTAGGGC 50
 Query Match 16
 Best Local Similarity 94.4%; Score 16.4%; DB 3; Length 68;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SEQ ID NO: 11
 LENGTH: 226
 TYPE: DNA
 ORGANISM: IN VITROGEN
 US-09-106-182-24

RESULT 16
 Sequence 9, Application US/09659026A
 Patent No. 6,461,616
 GENERAL INFORMATION:
 APPLICANT: MONTELARO, Ronald K.
 APPLICANT: CRAIGO, Jodi K.
 APPLICANT: ISSEL, Charlie
 APPLICANT: PUFFER, Bridget
 APPLICANT: HENNESSY, Kristina J.
 APPLICANT: BROWN, Karen K.
 TITLE OF INVENTION: EIAV P26 DELETION VACCINE AND DIAGNOSTIC
 FILE REFERENCE: MONTELARO ET AL.
 CURRENT APPLICATION NUMBER: US/09/659,026A
 CURRENT FILING DATE: 2001-06-11
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 9
 LENGTH: 226
 TYPE: DNA
 ORGANISM: IN VITROGEN
 US-09-659-026A-9

RESULT 17
 Sequence 24, Application US/09106182
 Patent No. 6,046,035
 GENERAL INFORMATION:
 APPLICANT: Shi, Yanggu
 APPLICANT: Rubin, Steve
 TITLE OF INVENTION: Cardiotrophin-Like Cytokine
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc
 STREET: 9410 Key West Ave
 CITY: Rockville
 STATE: MD
 COUNTRY: US
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/106,182
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/051,053
 FILING DATE: 30-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Brookes, A. Anders
 REGISTRATION NUMBER: 26,373
 REFERENCE/DOCKET NUMBER: PF385
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-309-8504
 TELEFAX: 301-309-8439
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 256 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 19
 Db 33 CTGGCGGAGTTAGGGC 50
 Db 33 CTGGCGGAGTTAGGGC 50
 Query Match 18
 Best Local Similarity 94.4%; Score 16.4%; DB 3; Length 256;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SEQ ID NO: 11
 LENGTH: 226
 TYPE: DNA
 ORGANISM: IN VITROGEN
 US-09-106-182-24

Matches	17;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	2	CTGGGGAGTGGGGC	19						
Db	123	CTGGGGAGTGGGGC	106						

Search completed: January 21, 2004, 13:11:50
Job time : 58 secs

This Page Blank (uspto)

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 10:59:47 ; Search time 1733 Seconds
 (without alignments)

294.515 Million cell updates/sec

Title: US-09-913-325-12
 Perfect score: 21
 Sequence: 1 gctggcggaggatggggcc 21
 Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0
 Searched: 22781392 seqs, 12152238056 residues
 Total number of hits satisfying chosen parameters: 455662784
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries
 Database : EST:
 1: em_estba:
 2: em_estchum:
 3: em_estin:
 4: em_estma:
 5: em_estov:
 6: em_estpl:
 7: em_estro:
 8: em_htc:
 9: gb_est1:
 10: gb_est2:
 11: gb_htc:
 12: gb_est3:
 13: gb_est4:
 14: gb_est5:
 15: em_estin:
 16: em_estom:
 17: em_gss_hum:
 18: em_gss_inv:
 19: em_gss_pln:
 20: em_gss_vrt:
 21: em_gss_fut:
 22: em_gss_mam:
 23: em_gss_mus:
 24: em_gss_pro:
 25: em_gss_rod:
 26: em_gss_phg:
 27: em_gss_prl:
 28: gb_gss1:
 29: gb_gss2:
 5: 21 100.0 145 10 AW904670 RCI-NN106
 6: 21 100.0 146 9 AR738045
 7: 21 100.0 150 13 BU72859
 8: 21 100.0 151 9 AA334384
 9: 21 100.0 151 12 BI055204
 10: 21 100.0 153 12 BI467181
 11: 21 100.0 157 12 BI467181
 c 12 21 100.0 159 12 BI040516
 13 21 100.0 169 9 A1523434
 14 21 100.0 169 9 A1691105
 15 21 100.0 171 10 BF97129
 16 21 100.0 171 10 BF919288
 17 21 100.0 172 9 AA215650
 18 21 100.0 172 10 BF932077
 c 19 21 100.0 174 9 AA615704
 20 21 100.0 174 10 BF374244
 21 21 100.0 174 10 BF702836
 22 21 100.0 176 10 BF64496
 23 21 100.0 176 12 BI040542
 24 21 100.0 177 12 BI040538
 c 25 21 100.0 179 10 AW668593
 26 21 100.0 179 12 BI040710
 27 21 100.0 181 12 BI040535
 c 28 21 100.0 182 10 AW668587
 29 21 100.0 183 14 CB048333
 c 30 21 100.0 183 14 CB048334
 c 31 21 100.0 184 9 AA433884
 32 21 100.0 185 12 BM94290
 33 21 100.0 185 14 R83374
 c 34 21 100.0 187 10 AW877945
 35 21 100.0 187 10 BE765800
 36 21 100.0 187 10 BE76185
 37 21 100.0 188 13 BU734617
 c 38 21 100.0 189 10 BF749857
 39 21 100.0 193 12 BI040729
 40 21 100.0 195 10 AW94698
 c 41 21 100.0 196 10 BF749861
 42 21 100.0 196 12 BI040731
 43 21 100.0 196 12 BI055202
 44 21 100.0 198 9 AW243998
 c 45 21 100.0 198 10 AW868592

ALIGNMENTS

RESULT 1
 H84500
 LOCUS Y002d12.s1 Soares fetal liver spleen INFUS Homo sapiens cDNA clone
 DEFINITION IMAGE:241559_3, similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);
 mRNA sequence.
 ACCESSION H84500
 VERSION 1
 KEYWORDS EST, Hemo sapiens (human)
 SOURCE Hemo Sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 121)
 AUTHORS Hillier,L., Clark,N., Dubroque,T., Elliston,K., Hawkins,M., Holman
 ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
 Raskin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
 ,R., Williamson,A., Wohldmann,P., and Wilson,R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished
 COMMENT Contact: Wilson.RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High Quality sequence starts: 1

SUMMARIES

Query Score Match Length DB ID Description

1 21 100.0 121 14 H84500 Y002d12.s1
 2 21 100.0 121 14 R93611 Yg3dd11.s1
 3 21 100.0 135 14 T53781 Yb83e02.s1
 c 4 21 100.0 143 10 BE76534 II3-NT010

Query Match	100	0%	Score 21;	DB 14;	Length 121;
Best Local Similarity	100.0%	Pred. No. 5.7e+02;			
Matches 21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Day	1	GTGGGGGAGTTGGGGCCT 21			
Db	95	GCTGGGGGAGTTGGGGCCT 115			
RESULT 2					
	R93611	121 bp	mRNA	linear	EST 29-AUG-1995
LOCUS	YGT8d11.s1	Soares fetal liver spleen INFSL	Homo sapiens	CDNA clone	
DEFINITION	IMAGE:18069_3,	similar to gb:K14723	CLUSTERIN PRECURSOR (HUMAN),		
		mRNA sequence.			
ACCESSION	R93611				
VERSION	R93611.1	GI:9677777			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
DEFINITION	Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Hillier,L., Clark,N., Dubique,T., Eilistron,K., Hawkins,M., Holman ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marr,M., Parsons,J., Riekin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston ,R., Williamson,A., Wohldmann,P., and Wilson,R.				
TITLE	The WashU-Merck EST Project				

COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 86 1800
Fax: 314 286 1810
Email: est@wustl.edu
Insert Size: 1368
High Quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (infoimage.lnl.gov) for further information.
Trace considered overall poor quality
Insert length: 1664 std error: 0.00

FEATURES	source	BASE COUNT	ORIGIN	Query Match	Best Local Similarity	Score	Match
Seq primer: Promega -21m13 High quality sequence scop: 1. Location/Qualifiers	1. .121 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:3767119" /db_xref="Taxon:9606" /clone="IMAGE:198069" /sex="male" /dev_stage="20 week-post lab host:DH10B (ampicil /clone_lib="Soares fetal /note="Organ: Liver and with a modified Polylink 1st strand cDNA was primed [5', AACTGGAAATTAAATTAAT double-stranded cDNA was (Pharmacia), digested with and Eco RI sites of the went through one round of constructed by Bento Soa 23 a 22 c 50 g 21 21 21 21						

RESULT 3		T53781		135 bp		mRNA		EST 06-FEB-1995	
Qy	1 GCTGGCGGAGTTGGGGCT 21	DEFINITION		y93e02.s1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:77863, similar to similar to gb:XI4723 CLUSTERIN PRECURSOR (HUMAN), mRNA sequence.					
Db	85 GCTGGCGGAGTTGGGGCT 105	ACCESSION		T53781		EST.		T53781.1 GI:65542	
KEYWORDS		SOURCE		Homo sapiens (human)		ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		AUTHORS		Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBudge,T., Favre,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlung,T., Schellenbeck,K., Soares,M.B., Tan,P., Thierry-Mieg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Watson,R., Wilson,R., and Marra,M.		TITLE		Generation and analysis of 280,000 human expressed sequence tags	
MEDLINE		JOURNAL		Genome Res. 6 (9), 807-828 (1996)		PUBMED		97044478	
PUBMED				8889549					

CONTACT: WILSON, K.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson@wustl.edu
Insert Size: 1905
High quality sequence starts: 1
Source: IMAGE Consortium, LILN This clone is available royalty-free
through LILN, contact the IMAGE Consortium (info@image.lnl.gov)
for further information. Trace considered overall poor quality
Insert Length: 1905 Std Error: 0.00
Seq primer: -21ml3
High quality sequence stop: 1.
location/quality="

RESULT 3		T53781		135 bp		mRNA		EST 06-FEB-1995	
Qy	1 GCTGGCGGAGTTGGGGCT 21	DEFINITION		y93e02.s1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:77863, similar to similar to gb:XI4723 CLUSTERIN PRECURSOR (HUMAN), mRNA sequence.					
Db	85 GCTGGCGGAGTTGGGGCT 105	ACCESSION		T53781		EST.		T53781.1	
		KEYWORDS		GI:65542		SOURCE		Homo sapiens (human)	
		ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
		REFERENCE		1 (bases 1 to 135)		AUTHORS		Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBudge,T., Favale,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlung,T., Schellenbeck,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E., Underwood,K., Whitedmann,P., Watson,R., Wilson,R., and Marra,M.	
		TITLE		Generation and analysis of 280,000 human expressed sequence tags		MEDLINE		97044478	
		JOURNAL		Genome Res. 6 (9), 807-828 (1996)		PUBMED		8889549	

CONTACT: WILSON, K.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson@wustl.edu
Insert Size: 1905
High quality sequence starts: 1
Source: IMAGE Consortium, LILN This clone is available royalty-free
through LILN, contact the IMAGE Consortium (info@image.lnl.gov)
for further information. Trace considered overall poor quality
Insert Length: 1905 Std Error: 0.00
Seq primer: -21ml3
High quality sequence stop: 1.
location/quality="

source 1. 135
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="QDB:497531"
 /db_xref="taxon:9606"
 /clone="IMAGE:7786"
 /sex="male"
 /dev_stage="49 years old"
 /lab_host="SOLR cells (Kanamycin resistant)"
 /clone_lab="Stratagene liver (#93724)"
 /note="Organ: liver; Vector: pBlueScript SK; Site: 1; ECOLI Site: 2; XbaI; Cloned unidirectionally. Primer: -Oligo dT. Hepatectomy from normal male caucasian. Average insert size: 1.1 kb. Uni-ZAP XR Vector; ~5' adapter sequence: 5', GAATTCGCAAGAG 3', -3' adapter sequence: 5', CTCGAGTTTTTTTTTTTT 3'"
 BASE COUNT 30 a 23 c 48 g 32 t 2 others
 ORIGIN

Query Match 100.0%; Score 21; DB 14; Length 135;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTGGGGAGTTGGGGCT 21
 Db 110 GCTGGGGAGTTGGGGCT 130

RESULT 4
 BE765434/c
 LOCUS TL3-NT0104-200500-144-G04 NT0104
 DEFINITION Homo sapiens cDNA, mRNA sequence.
 ACCESSION BE765434
 VERSION EST
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. (bases 1 to 143)
 REFERENCES 1 (bases 1 to 143)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Matsuoka, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?i1=&t2=RC1-NN1062-260400-01-a09&t3=2000-04-26&t4=1>)
 Seq. Primer: PUC 18 forward
 High quality sequence start: 34
 High quality sequence stop: 145.
 FEATURES source 1. 145
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NT0104"
 source 1. 143
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NT0104"
 BASE COUNT 20 a 31 c 61 g 33 t
 ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 143;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCTGGGGAGTTGGGGCT 21
 Db 102 GCTGGGGAGTTGGGGCT 82

RESULT 5
 AW904670
 LOCUS AW904670
 DEFINITION RC1-NN1062-260400-011-a09 NT01062
 ACCESSION AW904670
 VERSION AW904670.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Matsuoka, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?i1=&t2=TL3-NT01062-260400-01-a09&t3=2000-04-26&t4=1>)
 Seq. Primer: PUC 18 forward
 High quality sequence start: 8
 High quality sequence stop: 143.
 FEATURES source 1. 143
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NT0104"
 BASE COUNT 20 a 31 c 61 g 33 t
 ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 145;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0;

Qy 1 GCTGGGGGGAGTGGGGGCT 21
 Db 50 GCTGGGGGGAGTGGGGGCT 70

RESULT 6
 AA738045 LOCUS AA738045 linear EST 22-JAN-1998
 DEFINITION NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1256199 3,
 similar to 9b:X4723 CLUSTERIN PRECURSOR (HUMAN); mRNA sequence.

ACCESSION AA738045
 VERSION AA738045.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 150)
 AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 8889548
 PUBLMED
 COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road,
 Iowa City, IA 52242, USA
 Email: bento-soares@uiowa.edu
 Tissue Procurement: Dr. Greg Hageman
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.rgen.com).
 Seq primer: M13 FORWARD
 POLYA:yes.

FEATURES Source
 1. 150
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="exon:9606"
 /clone="UI-B-CQ0-adv-g-07-0-UI"
 /tissue_type="optic nerve"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-B-CQ0 is a cDNA library containing the following tissue(s): optic nerve. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the 'TGT'18 tail. The sequence tag for this library is CCATTAATG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
 TAC_LIB=UI-B-CQ0
 TAG_TISSUE=human optic nerve
 TAG_SEQ=CCATTAATG"
 BASE COUNT 31 a 24 c 47 g 48 t
 ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 146;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0;

Qy 1 GCTGGGGGGAGTGGGGGCT 21
 Db 106 GCTGGGGGGAGTGGGGGCT 126

RESULT 7
 BUT28259 Locus BU728259 linear EST 09-OCT-2002
 DEFINITION UI-B-CQ0-adv-g-07-0-UI.s1 Homo sapiens cDNA clone.
 ACCESSION UI-B-CQ0-adv-g-07-0-UI 3, mRNA sequence.
 VERSION BU728259
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 150)
 AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 8889548
 PUBLMED
 COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road,
 Iowa City, IA 52242, USA
 Email: bento-soares@uiowa.edu
 Tissue Procurement: Dr. Greg Hageman
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.rgen.com).
 Seq primer: M13 FORWARD
 POLYA:yes.

FEATURES Source
 1. 150
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="exon:9606"
 /clone="UI-B-CQ0-adv-g-07-0-UI"
 /tissue_type="optic nerve"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-B-CQ0 is a cDNA library containing the following tissue(s): optic nerve. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the 'TGT'18 tail. The sequence tag for this library is CCATTAATG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
 TAC_LIB=UI-B-CQ0
 TAG_TISSUE=human optic nerve
 TAG_SEQ=CCATTAATG"
 BASE COUNT 31 a 24 c 47 g 48 t
 ORIGIN

Query Match 100.0%; Score 21; DB 13; Length 150;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0;

Qy 1 GCTGGGGGGAGTGGGGGCT 21
 Db 126 GCTGGGGGGAGTGGGGGCT 146

PUBLISHED	10737800	COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Fax: +55-11-27049221 Email: asimpson@ludwig.org.br	FEATURES	source	obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu) High quality sequence stop: 142.	
		LOCATION/QUALIFIERS	1. 157 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /issue_type="Purified pancreatic islet" /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: Not I; Site_2: Xhol; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' Xhol site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."				
		FEATURES	source	1. /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_lib="NT0232" /note="Organ: nervous tumor; Vector: pUC18; Site 1: Small; Site 2: Small; A mini-library was made by cloning products derived from OBESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under 1 low stringency conditions." 17 a 36 c 67 g 33 t	BASE COUNT	35 a 28 c 56 g 38 t	
		ORIGIN		RESULT 12 BI040516 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Query Match 100.0%; Score 21; DB 112; Length 157; Best Local Similarity 100.0%; Pred. No. 5.7e+02; Homo sapiens cDNA, mRNA sequence. B1040516 B1040516 1 GI:14447142 Homo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 159) REFERENCE AUTHORS Nagai,M., Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.P., Carvalho,A.F., Matsuoka,A., Baia,G.S., Simpson,D.H., Goldman,G.H., Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,P., Brentani,R.B., Reis,L.F., de Souza,S.J., and Simpson,A.J.	RESULT 12 BI040516 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Query Match 100.0%; Score 21; DB 112; Length 159 bp, mRNA, linear EST 14-JUN-2001 B1040516 B1040516 1 GI:14447142 Homo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 159) REFERENCE AUTHORS Nagai,M., Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.P., Carvalho,A.F., Matsuoka,A., Baia,G.S., Simpson,D.H., Goldman,G.H., Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,P., Brentani,R.B., Reis,L.F., de Souza,S.J., and Simpson,A.J.
		ORIGIN		RESULT 11 BI1467181 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Query Match 100.0%; Score 21; DB 12; Length 153; Best Local Similarity 100.0%; Pred. No. 5.7e+02; Homo sapiens CDNA 3', mRNA sequence. B11467181 B11467181 1 GI:15280059 Homo sapiens (human) Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. Metabolism, Biotransformation, and Cellular Biology, Cambridge, MA, Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y., and Bowers,Y. Endocrine Pancreas Consortium Unpublished Other ESTs: ic19a12.y3	RESULT 11 BI1467181 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Query Match 100.0%; Score 21; DB 12; Length 157 bp, mRNA, linear EST 22-AUG-2001 B11467181 B11467181 1 GI:15280059 Homo sapiens (human) Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. Metabolism, Biotransformation, and Cellular Biology, Cambridge, MA, Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y., and Bowers,Y. Endocrine Pancreas Consortium Unpublished Other ESTs: ic19a12.y3
		COMMENT	Contact: Douglas Meitzen, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-495-1812 Fax: 617-495-8857 Email: dmelton@biohup.harvard.edu Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For Information on	JOURNAL COMMENT	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) COMMENT Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-27049222 Fax: +55-11-27070011 Email: asimpson@ludwig.org.br	FEATURES	source /organism="Homo sapiens" 1. 159

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 171)

REFERENCE Dias Neto, E., Garcia Correa, R., Verjovskii-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brustein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 2002663

PubMed 10137800

COMMENT Contact: Simpson A.J.G.
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01050-010, São Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LIGR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethm12.pl?t1=IL0&t2=IL0-MT0215-281100-501-all&t3=2000-11-28&t4=1>)

Seq primer: puc 18 forward
 H:igh quality sequence stop: 171.

FEATURES

Source
 1. .171
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="trixon19606"
 /dev_stage="Adult"
 /clone_lib="MT0215"
 /note="Organelle: marrow; Vector: puc18; Site_1: Small; Site_2:
 Small; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No. 196
 7116 - Ludwig Institute for Cancer Research) profiles
 into the PUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

BASE COUNT
 ORIGIN

Query Match 100.0% Score 21; DB 10; Length 171;
 Best Local Similarity 100.0% Pred. No. 5.7e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGGGAGTGGGGCT 21
 Db 21 GCTGGGGAGTGGGGCT 41

Search completed: January 21, 2004, 13:09:47
 Job time : 1739 secs